

BEST AVAILABLE COPY

Figure 1

Motif 0

AKFLHHLMSVYVVELRSPFFYVTETTFQKNR  
ISEIE-LWLCXRGNAXMCLSDFEKQKQIFAEFYIYLYNSPIIPILQSFYITESSDLRNR  
LXDFRWLFISD---IWFTKXNFENLNQLAICFISWLPQOLIPKIIQTFFYCTEISSTVT-  
TREISTHQVET-SAXHPYFFDHEN-LYVLWKLRLWIFEDLVVSLRCFFYVTEQQKSYXK  
.....

Motif 1

LPFYKSVWSKLQSTIGTRQHLXRVQLRDVSEAZVRQHRARPALLTSRLRFIPKP--COL  
TVYFRKDIWKLRCRFFI-TSHKMEAFERINENNVRMDTQK-TTLPPAVIRLLPKK--STP  
IWIYFRHDTWKKLITPFIYEYFKTYLWENWVCRNHNSTLS--HFNHSHKRIIPKKSHEF  
TYYRKNHWDVIMKHSI-ADLKKETLAEVQEKVEBWKKS-LGFAPGKLRLIPKK--TTF  
.....

Motif 2

RPIVNMHDYVVGARTFRERKRAERLTSRVKALP-SVLNYERA  
RLITH-LRXRFLLKMGSHKXKMLVSTNQTLPVASILXHLIWEESSTPFFHLEVYMKLLTF  
RTIAIPCRGADEEFTIYKENHKKWAIQPTQKILEYLRNKRPTSTFKIYSPTQIADRIKEF  
RPIHTFHKKIVNSDRKTTKLTHTKLLSHLHLXTLKN-RHFKDPPCPAVFNHDDVHKKY  
..

Motif 3 (A)

KKDLLKMRHFGK-KXYFVRIDIKSCYDRIKQDLMFRIVKK-KLYDPEPVIRKYATIHATS  
KQRLKXKFNNVLPZLYFMKFDVKSCYDSIPRMECHRILKD-ALKNENGFFVRSQYFFSTN  
EEFVCKXWKQVCQPKLFFATHDIEKCYDSVNREKLSTFLKTTXLLSSDFWIMTAQILKXKY  
.....

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Human  
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Figure 2

69432500  
602207  
60522460

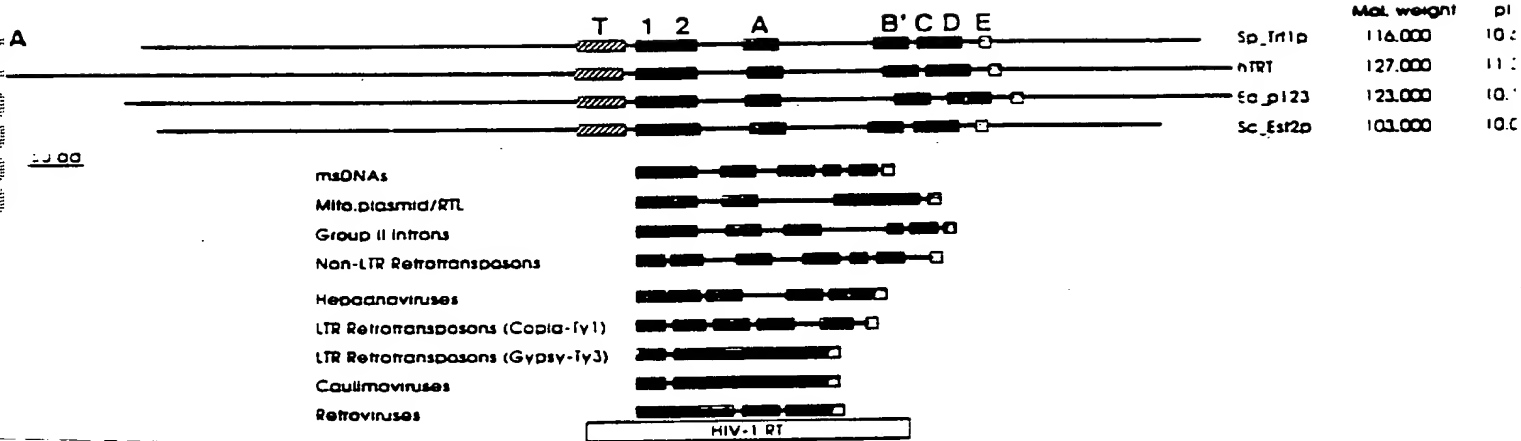
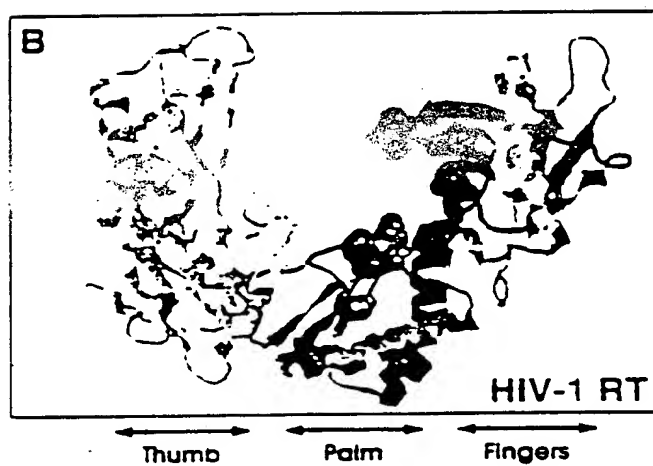


Figure 3



**6079**

**Motif T**

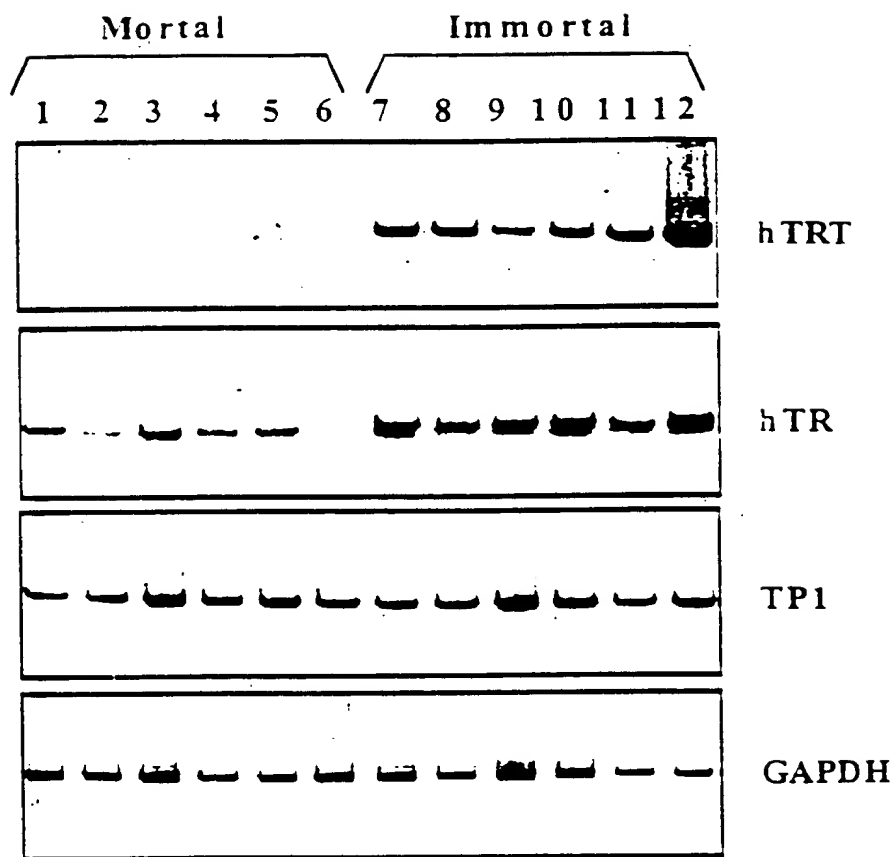
TRT con	WL	hh	hh	pfyy	ts	p	n	y	rk	w	l	h	x	km	
Sp_Trt1p	429	WL	YNSF	IIPI	LS	YIT	SSDL	RNP	Y	Y	P	R	I	Y	8
bTRT	546	WLS	VYV	V	ELL	R	S	Y	Y	T	T	F	Q	K	10
Ea_p123	441	W	I	P	E	D	L	V	S	L	I	R	T	T	
Se_Est2p	366	W	L	F	R	O	L	P	K	I	K	I	O	T	8

Motif 1		Motif 2		Motif A	
TRT con	h hshlPKK p	FRhI h h K		PeLYTh hsh CTD I	hsh K
Bp_Trt1p	NNVRMDTKTKTLPPAVIHLFPKPT	FLPILTNLRKRLFIOMSGNIOQLVSTNOTL	40	FGRLTKTVRIDIKSTDRIKODLMFRIVKGLKD	80
hTRT	EVROHREARPALLLSRLEFIPKPGD	LRPZVMNDYVVGARTFRREKRAERLTSRV	43	PPPELYTVFKVDVTGAYDTIPODRLTEVIASIKP	87
Se_p123	KEVEEWKSLGFAPGKRLRLIPKTT	FRPZMTFNKKIVNSDRKTKLTNTKLLN	41	GQPKLFTATHDIKCYDSVNRKLSLFTLTKLL	100
Se_Sat2p	CRNHNSYTLSSNFNHSKRIIPKSSNN	FPIAIPCRGADEEEFTPIKENHKAIOF	42	VLPELYPKFPDVKSCYDSIPRMECHRIKDALDN	62
					AF
RT con	p hh h K	hR h K		h hsh SF n	
Se_a1	LSNLGCTGPKFKPKRIIVNFKPKGG	IRPLSVGNPKDRKIVQEVMMILDTIFDK	27	FGGSMNPIEVDLKCFDTTSHDLIKELKRYISD	20
Db_TART	SILRIGYYPDAWKHAGVOMLKPGRS	YRPISLISGLSRPFRLLRLFRVDFLK	32	KRYCYSAPVLDISEAFDRVWHGELLKLAIKILPY	25
BIV-1	EGKISKIGPENPYNTPVFAIKKQDST	WRKLVDPRELNKRTQDFWEVQLGIPHPAG	0	LKKKSVTVLDVGDATFSVPLDEDFRKTYAFTIP	

	Motif B'	Motif C	Motif D	Motif E
TRT con	K Y Q Q GIPOGS LS hL h Y DL F	LLRL DDFLhIT	A F L h G c p N cK	W G S
Sp_Trt1p	SOYLQKVGIPGGSILBSFLCYMEDLIDEYLSST	LLRLVDDFLFIVNKKD 0	AKKFLNLSLGPEKHNKFNSTSLFIVT 17	KRRMFFGFSV 181
hTRT	KSYVOCQGIPOGSILSLTLLCSLCSDHKNKLFAGI	LLRLVDDFLFIVPHLTH 0	AKKFLRTLVRGVPYEGCVBLRLTVV 19	HGLFPMGCLLL 197
Ra_p123	KFTKQTKGIPOGLCVBSLSSFFYATLEESSLGFL	LLRLTDDYLLITPTQENN 14	AVLFI EKLINVSRENGPKFKDKLLO 20	QDYCDWKGISI 179
Ra_Est2p	KCIYREDLGIPGGSLSAPIVDLVDLLEFYSEK	ILKLADDFLIISTDQOO 0	VINIKKLANNFGPKYNAKANRDLAT 23	KELEVWKSST 146
		F		
RT con	hPQG pP hh h	h Y DDDhh	Gh h cK h	hLG h
Sa_a1	TYHKHPLGLPGSILSLPLCNIVMTLVDNLEDYI	YVYADDILIGVLGSKS 2	KMKRRDLNNGFN-LGLTLSEEEKTLI 4	ETPARFLGYST 1
Dm_TART	RAGQIAGGVPGSGNLGPILYSFSSDNLPHIHYH	LSYADDITVLSSDILA 6	NNYLIKTPSDWADKNGISVBAAKTCH 25	ESKQSYLGVIL
HIV-1	RIYQYVNLVPGQWKGSPAIFQSSHTKILEPFFKON	IYQYDDYLVGSDLEIG 4	HRTKIEELRHLRLRWGLTTPDKKHQK 1	EPFFLWKGITL
	▲	▲	▲	▲

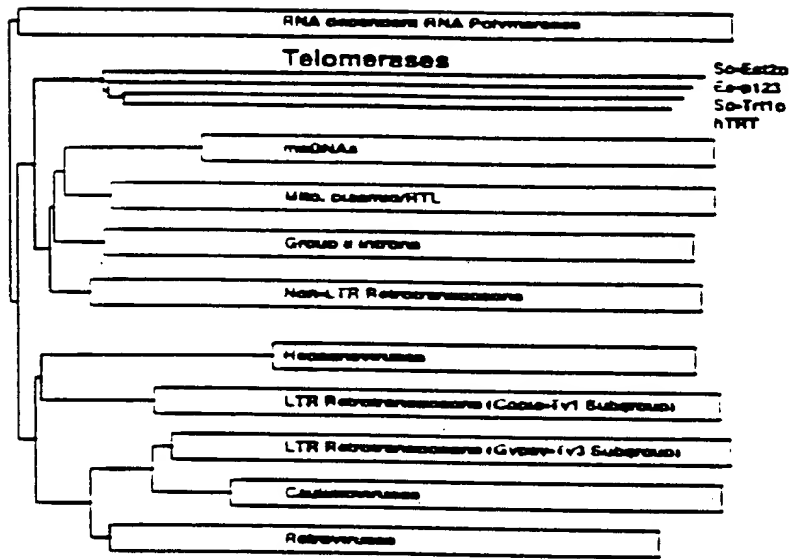


Figure 5



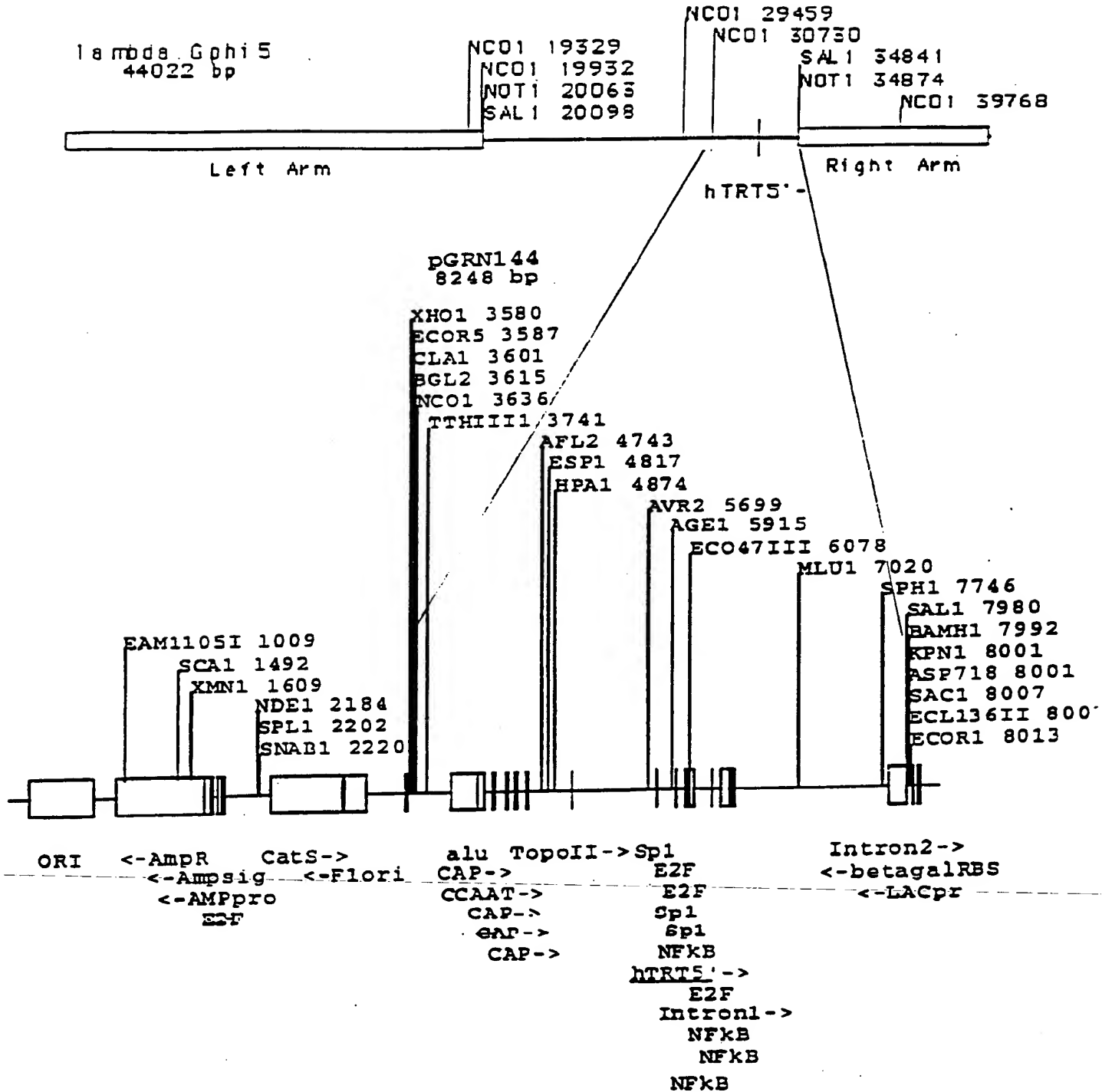
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Figure 6



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Figure 7



TopoII Cleavage Site

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Figure 8

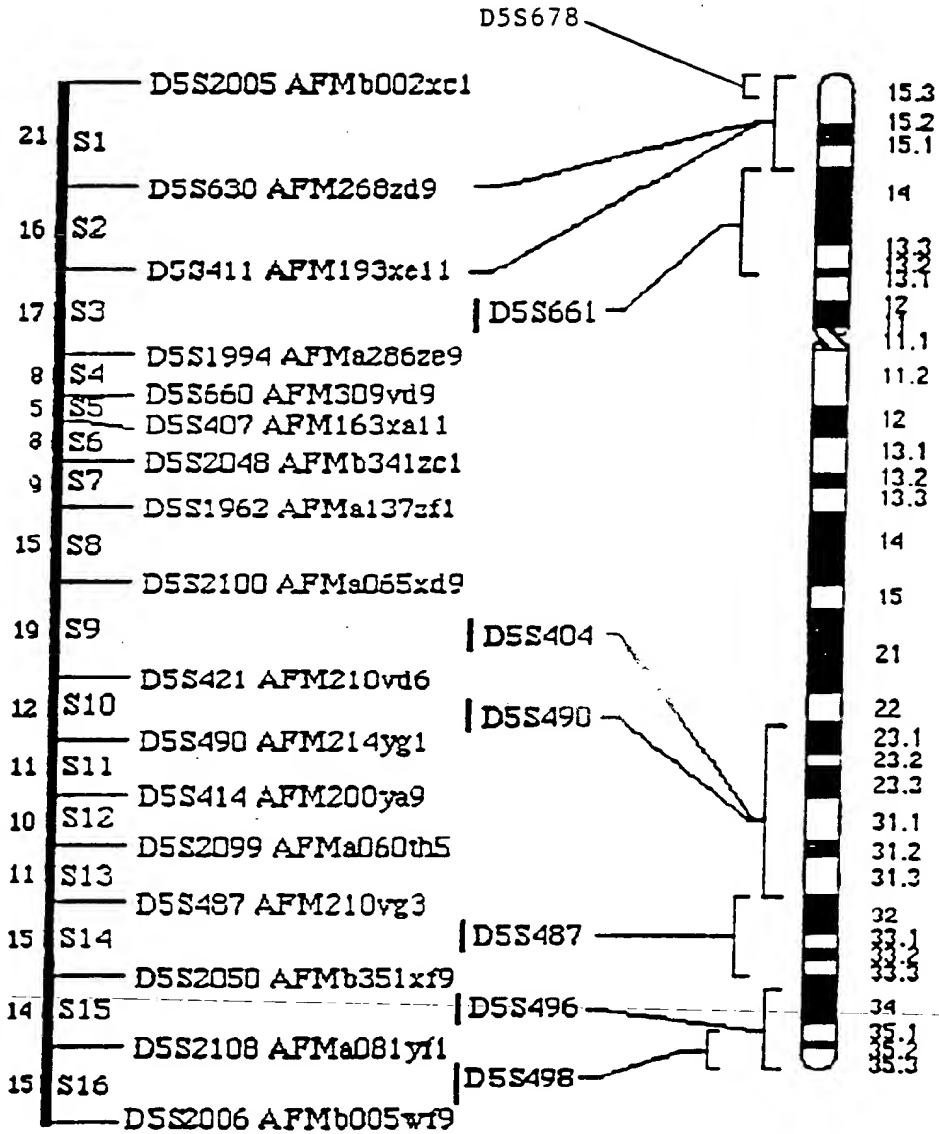
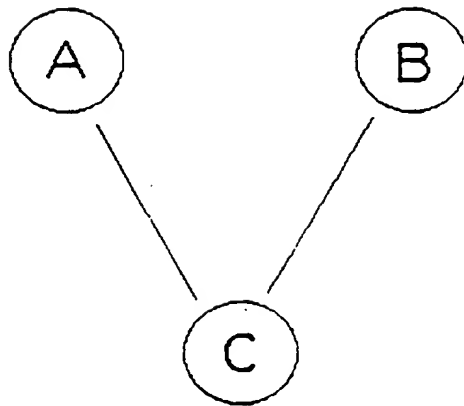
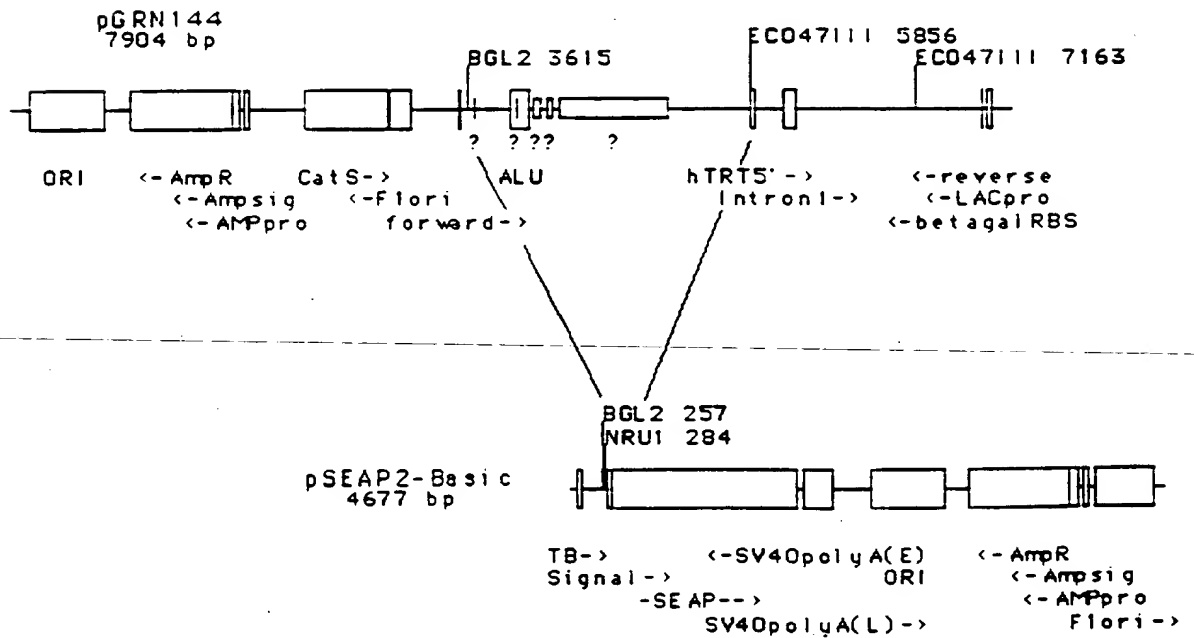


FIGURE 9

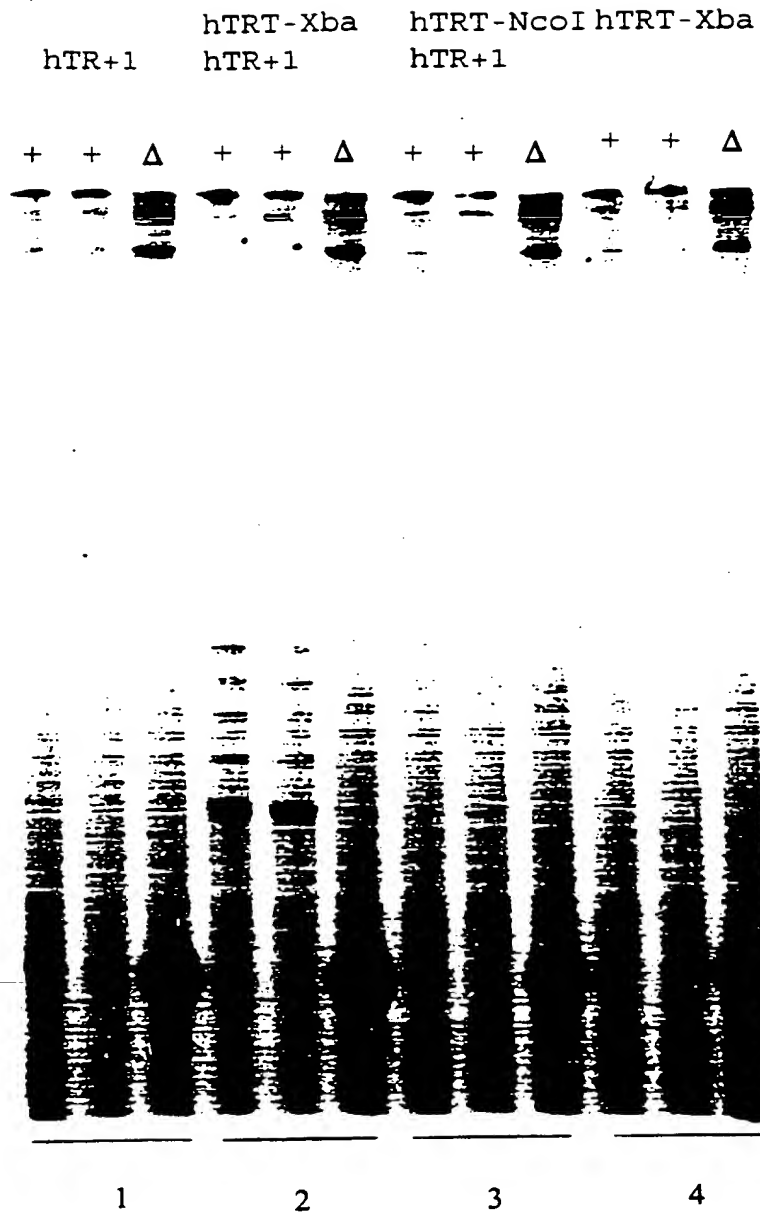
# Promoter Reporter Construct



A = pGRN144  
 B = pSEAP2-Basic  
 C = BGL2-ECO47111 fragment from A  
 into BGL2-NRU1 sites of B.



Page 1



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Figure 10  
Page 2  
Reticulocyte  
Lysate

hTERT NcoI Reticulocyte  
Lysate

+ + Δ + + Δ

↑ pCT  
↑ other

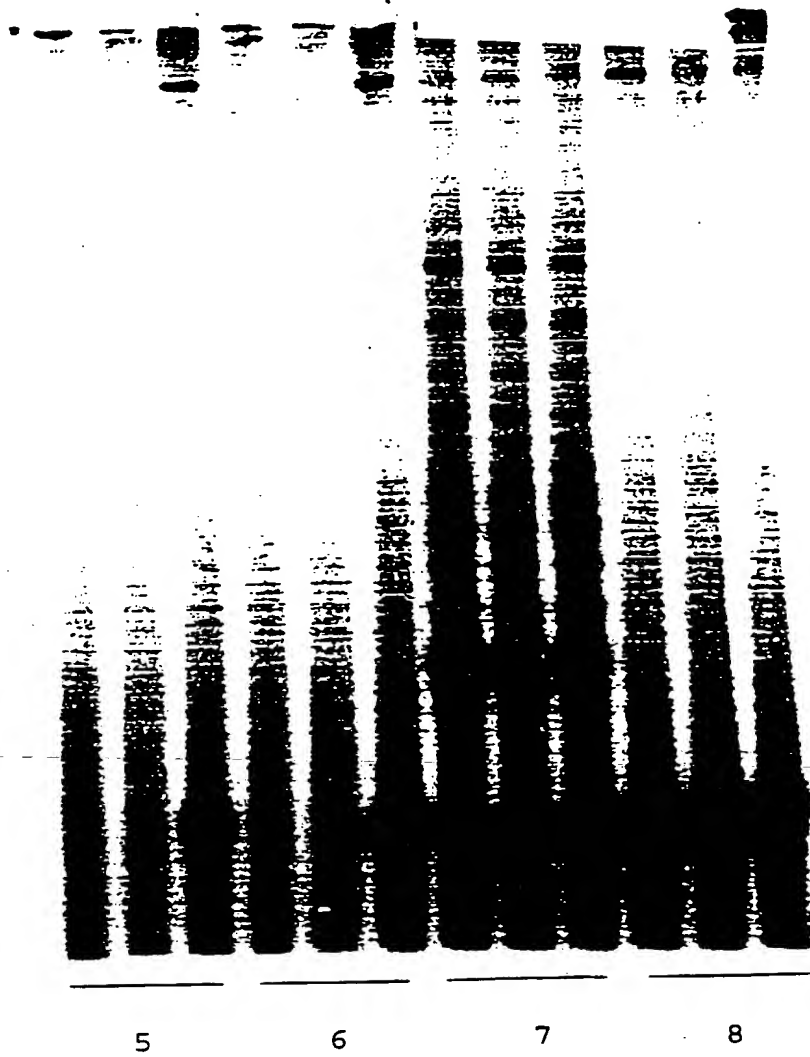


FIGURE 11

Page 1

# Telomerase Specific Motifs

	MOTIF T	MOTIF T'
TRT con	FFY TE	E V
hTRT	W1	
spTRT	546 WLM SVVVELLR SFYV TETTFQKNRLFFYRKSVWSKLQSIGI 13 EAEVR	
Ea_p123	429 WLYNSFIIPILQSFYITESSDLNRNTVYFRKDIWKLCPFI 12 ENNVR	
Sc_Est2	441 WIFEDLVSLIRCFYVTEQQKSYSKTYYYRKNIDVIMKMSI 12 EKEVE	
	366 WLFRLIPKIIQTFYCYTEISSTVT.IVYFRHDTWNKLITPFI 9 ENNVC	

# Telomerase RT Motifs (Fingers)

	MOTIF 1	MOTIF 2	MOTIF A	MOTIF B'
TRT con	R iPKk	fr I	p lyF D CYD i	Y q GIPQGs lS l Y
hTRT	11 SRLRFIPKPDG 0 LRPIV	69 PELYFVKVDVTGAYDTI 104 YVQCQGIPQGSILSTLLCSLCY		
spTRT	10 AVIRLLPKKNT 0 FRLIT	66 RKKYFVRIDIKSCYDRI 99 YLQKVGIPOGSILSSFLCHFYM		
Ea_p123	10 GKRLIPKKT 0 FRPIM	67 PKLFFATMDIEKCYDSV 117 YKQTKGIPQGLCVSSILSSFY		
Sc_Est2	13 SKMRIIPKKS 2 FRIIA	68 PELYFMKFDVKSCYDSI 85 YIREDGLFQGSLSAPIVDLVY		
RT con	p hh h K	h hDh AF h	hPQG pP hh h	
		GY		



# Telomerase RT Motifs (Palm, Primer Grip)

	MOTIF C	MOTIF D	MOTIF E
TRT con	111rl DDfL it	g	w g s l
hTRT	15 LLLRLVDDFLLVT	15 GVPEYGC	24 WCGLLLDTRTL
spTRT	16 VLLRVVDDFELFIT	15 GFEKHNF	22 FFGFSVNMRS
Ea_p123	24 LLMRLTDDYLLIT	15 VSRENGF	28 WIGISIDMKTL
Sc_Est2	18 LILKLADDFLIIS	15 GFQKYNAP	25 WKHSSTMNNFH
RT con	h Y DDhhh	Gh	hLG h
	F		

FIGURE 12

Seq. ID. No 7

181 GGACCCGCGCGCTTTCCGCGCGCTGGTGGCCCCAGTGCCTGGTGTGCGTGCCCTGGGACGC  
CCTGGGCCGCGCGAAAGGCGCGCGACACCAGGGTCACGGACCAACACGCACGGGACCCTGCG

NFkB\_CS1  
GGGRQTYYYQC  
NFkB-MHC-I.2  
TGGGCTTCCCC

241 ACGGCCGCCCCCGCGCGCCCCCTCCTTCCGCGCAGGTGGGCCTCCCCGGGGTCCGGCGTCCG  
TGCCGGCGGGGGCGCGCGGGGGAGGAAGGCGGTCCACCCGGAGGGGCCCCAGCCGCAGGC

Intron1

301 GCTGGGGTTGAGGGCGGCGGGGGGAACCGCGACATGCGGAGAGCAGCGCAGGCGACTC  
CGACCCCAACTCCCGCGCGCCCCCTTGGTCGCTGTACGCCTCTCGTCGCGTCCGCTGAG

NFkB\_CS1  
GGGRQTYYYQC  
NFkB\_CS2  
RGGGRMTYYCC  
Topo\_II\_cleavage\_site  
RNYNNCINNGYNGKTNYNY

361 AGGGCGCTTCCCCCGCAGGTGTCCTGCCTGAAGGAGCTGGTGGCCCCAGTGCTGCAGAGG  
TCCCGCGAAGGGGGCGTCCACAGGACGGACTTCCTCGACCACCGGGCTCACGACGTCTCC

66207 20523460

# Figure 13

Page 1

1 AAAACCCCAA AACCCCAAAA CCCCTTTTAG AGCCCTGCCAG TTGGAAATAT  
 51 AACCTCAGTA TTAATAAGCT CAGATTTTAA ATATTAATTA CAAAACCTAA  
 101 ATGGAGGTTG ATGTTGATAA TCAAGCTGAT AATCATGGCA TTCACTCAGC  
 151 TCTTAAGACT TGTGAAGAAA TTAAAGAAGC TAAAACGTTG TACTCTTGGG  
 201 TCCAGAAAGT TATTAGATGA AGAAATCAAT CTCAAAGTCA TTATAAAGAT  
 251 TTAGAAGATA TTAAAATATT TGCGCAGACA AATATTGTTG CTACTCCACG  
 301 AGACTATAAT GAAGAAGATT TTAAAGTTAT TGCAAGAAAA GAAGTATTTT  
 351 CAACTGGACT AATGATCGAA CTTATTGACA AATGCTTAGT TGAACCTTCT  
 401 TCATCAAGCG ATGTTTCAGA TAGACAAAAA CTTCAATGAT TTGGATTTCG  
 451 ACTTAAGGGA AATCAATTAG CAAAGACCCA TTTATTAACA GCTCTTTCAA  
 501 CTCAAAAGCA GTATTTCTTT CAAGACGAAT GGAACCAAGT TAGAGCAATG  
 551 ATTGGAAATG AGCTCTTCCG ACATCTCTAC ACTAAATATT TAATATTCCA  
 601 GCGAACTTCT GAAGGAACTC TTGTTCAATT TTGCGGGAAT AACGTTTTTG  
 651 ATCATTTGAA AGTCAACGAT AAGTTTGACA AAAAGCAAAA AGGTGGAGCA  
 701 GCAGACATGA ATGAACCTCG ATGTTGATCA ACCTGCAAAT ACAATGTCAA  
 751 GAATGAGAAA GATCACTTTC TCAACAACAT CAACGTGCCG AATTGGAATA  
 801 ATATGAAATC AAGAACCAGA ATATTTTATT GCACTCATTT TAATAGAAAT  
 851 AACCAATTCT TCAAAAAGCA TGAGTTTGTG AGTAACAAAA ACAATATTTT  
 901 AGCGATGGAC AGAGCTCAGA CGATATTCAC GAATATATTC AGATTTAATA  
 951 GAATTAGAAA GAAGCTAAAA GATAAGGTTA TCGAAAAAAT TGCCTACATG  
 1001 CTTGAGAAAG TCAAAGATTT TAACTTCAAC TACTATTTAA CAAAATCTTG  
 1051 TCCTCTTCCA GAAAATTGGC GGGAAACGGAA ACAAAAAATC GAAAACCTGA  
 1101 TAAATAAAAC TAGAGAAGAA AAGTCGAAGT ACTATGAAGA GCTGTTTAGC  
 1151 TACACAACTG ATAATAAATG CGTCACACAA TTTATTAATG AATTTTTCTA  
 1201 CAATATACTC CCCAAAGACT TTTTGACTGG AAGAAACCGT AAGAATTTTC  
 1251 AAAAGAAAGT TAAGAAATAT GTGGAACATA ACAAGCATGA ACTCATTCAC  
 1301 AAAAATTAT TGCTTGAGAA GATCAATACA AGAGAAATAT CATGGATGCA  
 1351 GGTTGAGACC TCTGCAAAGC ATTTTATTA TTTTGATCAC GAAAACATCT  
 1401 ACGTCTTATG GAAATTGCTC CGATGGATAT TCGAGGATCT CGTCGTCTCG  
 1451 CTGATTAGAT GATTTTTCTA TGTACCCGAG CAACAGAAAA GTTACTCCAA  
 1501 AACCTATTAC TACAGAAAGA ATATTTGGGA CGTCATTATG AAAATGTCAA  
 1551 TCGCAGACTT AAAGAAGGAA ACGCTTGCTG AGGTCCAAGA AAAAGAGGTT  
 1601 GAAGAATGGA AAAAGTCGCT TGGATTTGCA CCTGGAAAAC TCAGACTAAT  
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 2001 CTGCACAAAT TCTAAAGAGA AAGAATAACA TAGTTATCGA TTCGAAAAAC  
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 2251 CCAATATAAT TACATTAAT TTAATGGGAA GTTTTATAAA CAAACAAAAG  
 2301 GAAATCCTCA AGGTCTTGA GTTTCATCAA TTTTGTGATC ATTTTATTAT

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# Figure 13

Page 2

2351 GCAACATTAG AGGAAAGCTC CTTAGGATTC CTTAGAGATG AATCAATGAA  
2401 CCCTGAAAAT CCAAATGTTA ATCTTCTAAT GAGACTTACA GATGACTATC  
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2501 ATAAACGTAA GTCGTGAAAA TGGATTTAAA TTCAATATGA AGAAACTACA  
2551 GACTAGTTTT CCATTAAGTC CAAGCAAATT TGCAAAATAC GGAATGGATA  
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2751 CAATGTGGCT CAAGAAGAAA CTAAAGTCGT TTTTAATGAA TAACATTACC  
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3101 AAGTACATTT TCAACAGAGT TTGCATGATC CTCAAGGCCAA AAGAAGCAAA  
3151 CCTAAAAAGT GACCAATGTC AATCTCTAAT TCAATATGAT GCATAGTCGA  
3201 CTATTCTAAC TTATTTTGA AAGTTAATTT TCAATTTTGG TCTTATATAC  
3251 TGGGGTTTTG GGGTTTTGGG GTTTTGGGG

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Figure 14

MEVDVDNQAD NHGIHSALKT CEEIKEAKTL YSWIQKVIRC RNOSQSIFYKD  
51 LEDIKIFAQT NIVATPRDYN EEDFKVIARK EVFSTGLMIE LIDKCLVELL  
101 SSSDVSDRQK LQCFGFQKLG NOLAKTHLLT ALSTQKQYFF QDEWNQVRAM  
151 IGNELFRHLY TKYLIFQRTS EGTLVQFCGN NVFDHLKVND KFDKKQKGGGA  
201 ADMNEPRCCS TCKYNVKNEK DHFLNNINVP NWNMMKSRTR IFYCTHFNRN  
251 NQFFKKHEFV SNKNNISAMD RAQTIFTNIF RFNRIRKKLK DKVIEKJAYM  
301 LEKVKDFNFN YYLTNSCPLP ENWRERKQKI ENLINKTREE KSKYYEELFS  
351 YTTDNKCVTQ FINEFFYNIL PKDFLTGRNR KNFQKKVKKY VELNKHLEH  
401 KNLLLEKJNT REISWMQVET SAKHFYYFDH ENYVLWKLL RWTFEDLVVS  
451 LIRCFYVTE QQKSYSKTTY YRKNIWDVIM KMSIADLKKE TLAEVQEKEV  
501 EEWKKS LGFA PGKLR LIPKK TTFRPIMTFN KKI VNSDRKT TKLTTNTKLL  
551 NSHMLMLKTLK NRMFKDPFGF AVFNYDDVMK KYEEFVCKWK QVGQPKLFFA  
601 TMDIEKCYDS VNREKLSTFL KTTKLLSSDF WIMTAQILKR KNNIVIDSKN  
651 FRKKEMKDYF ROKFQKJALE GGQYPTLFSV LENEQNDLNA KKT LIVEAKO  
701 RNYFKKDNLL QPVNICQYN YINFNGKFYK QTKGIPQGLC VSSILSSFYY  
751 ATLEESSLGF LRDESMNPEN PNVNLLMRLT DDYLLITTQE NNAVLFIEKL  
801 INVSRENGFK FNMKKLOTSE PLSPSKFAKY GMDSVEEQNI VQDYCDWIGI  
851 SIDMKTLALM PNINLRIEGI LCTNLNLMQT KKASMWLKKK LKSFLMNTT  
901 HYFRKTTTTE DFANKTLNKL FISGGYKYMQ CAKEYKDHFK KNLAMSSMUD  
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0943500 11030  
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# Figure 15

Page 1

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959  ATG ACC GAA CAC CAT ACC CCC AAA AGC AGG ATT CTT CGC TTT CTA GAG AAT CAA TAT GTA 1018
      1 M T E H H T P K S R I L R F L E N Q Y V 20

1019  TAC GTA TGT ACC TTA AAT GAT TAT GTA CAA CTT GTT TTG AGA GGG TCG CCC GCA AGC TCG 1078
      21 Y L C T L N D Y V Q L V L R G S P A S S 40

1079  TAT AGC AAT ATA TCC GAA CCC TTG AGA AGC GAT GTA CAA ACC TCC TTT TGT ATT TTT CTT 1138
      41 Y S N I C E R L R S D V Q T S F S I F L 60

1139  CAT TCG ACT GTA GTC GGC TTG GAC AGT AAG CCA GAT GAA GGT GTT CAA TTT TGT TGT CCA 1198
      61 H S T V V G F D S K P D E G V Q F S S P 80

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	86		
	1273	CTA ATA GCC AAT GTT GTA AAA CAG ATG TTC GAT GAA AGT TTT GAG COT CGA AGG AAT CTA	1332
	97	L I A N V V K Q M F D E S F E R R R N L	106
	1333	CTC ATG AAA GCG TTT TCC ATG gttaaggatcttaccgtgaacaaccttacctgcaactaccgtcccagaaga	1405
	107	L M K G F S M	113
	1406	cctgataccaaccgacaaaag AAT CAT GAA GAT TTT CGA GCC ATG CAT GTA AAC GGA GTA CAA AAT	1469
	114	N H E D F R A M H V N G V Q N	128
	1470	GAT CTC GTT TCT ACT TTT CCT AAT TAC CTT ATA TCT ATA CTT GAG TCA AAA AAT TGG CAA	1529
	129	D L V S T F P N Y L I S I L E S K N W Q	148
	1530	CTT TTG TTA GAA AT gtaaatacccggttaagatgttgggcacctttaaacaaagactgacaagtataag T ATC GGC	1601
	149	L L L E I	I G 155
	1602	ACT GAT CCC ATG CAT TAC TTA TTA TCC AAA GGA AGT ATT TTT GAG COT CTT CCA AAT GAC	1661
	156	S D A M H Y L L S K G S I F E A L P N D	175
	1632	AAT TAC CTT CAG ATT TCT GGC ATA CCA CTT TTT AAA AAT AAT CTC TTT GAG GAA ACT CTC	1721
	176	N Y L Q I S G I P L F K N N V F E E T V	195
	1722	TCA AAA AAA ACA AAG CGA ACC ATT GAA ACA TCC ATT ACT CAA AAT AAA AGC GGC GGC AAA	1781
	196	S K K R R R T I E T S I T Q N K S A R K	215
	1782	GAA GTT TCC TGG AAT AGC ATT TCA ATT AGT AGG TTT AGC ATT TTT TAC AGG TCA TCC TAT	1841
	216	E V S W N S I S I S R F S I F Y R S S Y	235
	1842	AAG AAG TTT AAG CAA G gtaaccaataccggttatccctcataactaactccag AT CTA TAT TTT AAC	
	907		
	216	K K F K Q D	L Y F N 245
	1908	TTA CAC TGT ATT TGT GAT CCG AAC ACA GTA CAC ATG TGG CTT CAA TGG ATT TTT CCA AGG	1967
	246	L H S I C D R N T V H M W L Q W I F P R	265
	1968	CAA TTT GGA CTT ATA AAC GCA TTT CAA GTG AAG CAA TTG CAC AAA CTG ATT CCA CTC GTA	2027
	256	Q F G L I N A F Q V K Q L H K V I P L V	285
	2028	TCA CAG AGT ACA GTT GTG CCC AAA COT CTC CTA AAG GTA TAC CET TTA ATT GAA CAA ACA	2087
	286	S Q S T V V P K R L L K V Y P L I E Q T	305
	2088	GCA AAG CGA CTC CAT COT ATT TCT CTA TCA AAA GTT TAC AAC CAT TAT TGG CCA TAT ATT	2147
	06	A K R L H R I S L S K V Y N H Y C P Y I	325
	2148	GAC ACC CAC GAT GAT GAA AAA ATC CTT AGT TAT TCC TTA AAG CCG AAC CAG CTC TTT CCG	2207
	26	D T H D D E K I L S Y S L K P N Q V F A	345
	2208	TTT CTT CGA TCC ATT CTT GTT CGA GTG TTT COT AAA TTA ATC TGG COT AAC CAA AGG ATA	2267
	46	F L R S I L V R V F P K L I W G N Q R I	365
	2268	TTT CAG ATA ATA TTA AAA G gtaaccataaaaaacccacccacccacccacccacccac AC CTC GAA ACT	2336
	56	P E I I L K D	L F T 375

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	2337	TTC TGC AAA ATA TCG AGA TAC GAG TGT TTT AGT TTA CAT TAT TTA ATG AGT AAC ATA AAG	2396
176	F L K L S R Y E S F S L H Y L M S N I K	395	
	2397	gcacatcagcccaaatcttttcccctaactaacaaaccag ATT TCA GAA ATT GAA TGG CTA GTC CTT GGA	2465
396	I S E I E W L V L G	405	
	2466	AAA AGG TCA AAT GCG AAA ATG TGC TTA AGT GAT TTT GAG AAA CGC AAG CAA ATA TTT GCC	2525
406	K R S N A K M C L S D F E K R K Q I F A	425	
	2526	GAA TTC ATC TAC TGG CTA TAC AAT TCG TTT ATA ATA CCT ATT TTA CAA TCT TTT TTT TAT	2585
426	E F I Y W L Y N S F I I P I L Q S F F Y	445	
	2586	ATC ACT GAA TCA AGT GAT TTA CGA AAT CGA ACT GTT TAT TTT AGA AAA GAT ATT TGG AAA	2645
446	I T E S S D L R N R T V Y F R K D I W K	465	
	2646	C TC TTC TGC CGA CCC TTT ATT ACA TCA ATG AAA ATG GAA GCG TTT GAA AAA-ATA AAC GAG	2705
466	L L C R P F I T S M K M E A F E K I N E	485	
	2706	gtattttaaaaagtatttttttgcaaaaaagccaatacttttcag AAC AAT GTT AGG ATG GAT ACT CAG AAA ACT	2775
486	N N V R M D T Q K T	495	
	2776	ACT TTC CCT CCA GCA GTT ATT CGT GTA TTA CCT AAG AAG AAT ACC TTT CGT CTC ATT ACG	2835
496	T L P P A V I R L L P K K N T F R L I T	515	
	2836	AAT TTA AGA AAA AGA TTC TTA ATA AAG gtattaatttttgggcatcaatgaaccttaacttttaacctatta	2906
516	N L R K R F L I K	524	
	2907	ttagcgag ATG GGT TCA AAC AAA AAA ATG TTA GTC AGT ACC AAC CAA ACT TTA CGA CCT GTG	2967
525	M G S N K X M L V S T N Q T L R P V	542	
	2968	GCA TCG ATA CTG AAA CAT TTA ATC AAT GAA GAA AGT AGT GGT ATT CCA TTT AAC TTG GAG	3027
543	A S I L K H L I N E E S S G I P F N L E	562	
	3028	GTT TAC ATG AAG CTT CTT ACT TTT AAG AAG GAT CTT CTT AAG CAC CGA ATG TTT GG gtaac	3088
563	V Y M K L L T F K K D L L K H R M F G	581	
	3089	catacataatgccgcgatccccaccattaccaacttttcag G CGT AAG AAG TAT TTT GTA CCG ATA GAT ATA	3155
582	R K K Y F V R I D I	591	
	3156	AAA TCC TGT JAT GAT CGA ATA AAG CAA GAT TTC ATG TTT CCG ATT GTT AAA AAG AAA CTC	3215
592	X S C Y D R I K Q D L M F R I V K K K L	611	
	3216	AAG GAT CCC GAA TTT GTA ATT CGA AAG TAT GCA ACC ATA CAT GCA ACA AGT GAC CGA GCT	3275
612	K D P E F V I R K Y A T I H A T S D R A	631	
	3276	ACA AAA AAC TTT GTT AGT GAG GCG TTT TCC TAT T gtaaagtttatctttttcacctagggaattttttacaacaa	3343
632	T K N F V S E A F S Y F	643	
	3344	aactcccccttcag TT GAT ATG GTG CCT TTT GAA AAA GTC GTG CAG TTA CTT TCT ATG AAA ACA	3405
644	D M V P F E K V V Q L L S M K T	659	
	3406	TCA GAT ACT TTC TTT GTT GAT TTT GTG GAT TAT TCG ACC AAA AGT TCT TCT GAA ATT TTT	3465
660	S D T L F V D F V D Y W T K S S S E I F	679	
	3466	AAA ATG CTC AAG GAA CAT CTC TCT CGA CAC ATT GTT AAG gtatatcccaacttgtttgaactgtatacaaca	3532
680	K M L K E H L S G H I V K	692	



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1533	ctaatgaaactag	ATA GGA AAT TCT CAA TAC CTT CAA AAA GTT GGT ATC CCT CAG GGC TCA	1593
693		I G N S Q Y L Q K V G I P Q G S	708
3594	ATT CTG TCA TCT TTT TTG TGT CAT TTC TAT ATG GAA GAT TTG ATT GAT GAA TAC CTA TCG	3653	
709	I L S S F L C H F Y M E D L I D E Y L S	728	
3654	TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA GTA GTC GAC GAT TTC CTC TTT ATA ACA	3713	
729	F T K K K G S V L L R V V D D F L F I T	748	
3714	GTT AAT AAA AAG GAT GCA AAA AAA TTT TTG AAT TTA TCT TTA AGA G gtcagctctctgcatccc	3777	
749	V N K K D A K K F L N L S L R G	764	
3778	caagctctcaaccgttgaag GA TTT GAG AAA CAC AAT TTT TCT ACG AGC CTG GAG AAA ACA GTA	3840	
765	F E K H N F S T S L E K T V	778	
3841	ATA AAC TTT GAA AAT AGT AAT GGG ATA ATA AAC AAT ACT TTT TTT AAT GAA AGC AAG AAA	3900	
779	I N F E N S N G I I N N T F F N E S K K	798	
3901	AGA ATG CCA TTC TTG GGT TTC TCT GTG AAC ATG AGG TCT CTT GAT ACA TTG TTA GCA TCT	3960	
799	R M P F F G F S V N M R S L D T L L A C	818	
3961	GCT AAA ATT GAT GAA GGC TTA TTT AAC TCT ACA TCT GTA GAG CTG ACG AAA CAT ATG GGG	4020	
819	P K I D E A L F N S T S V E L T K H M G	838	
4021	AAA TCT TTT TTT TAC AAA ATT CTA AG gctaccctgctgaactgaataacagcttgacaaataactag A TCG	4089	
839	K S F F Y K I L R	848	
4090	AGC CTT GCA TCC TTT GCA CAA GTA TTT ATT GAC ATT ACC CAC AAT TCA AAA TTC AAT TCT	4149	
849	S L A S F A Q V F I D I T H N S K F N S	868	
4150	TGC TGC AAT ATA TAT AGG CTA GGA TAC TCT ATG TGT ATG AGA GCA CAA GCA TAC TTA AAA	4209	
869	C C N I Y R L G Y S M C M R A Q A Y L K	888	
4210	AGG ATG AAG GAT ATA TTT ATT CCC CAA AGA ATG TTC ATA ACG G gtcagtcacttattcttaactaga	4274	
889	R M K D I F I P Q R M F I T D	903	
4275	aaagctcttaactaaccctag AT CTT TTG AAT GTT ATT GGA AGA AAA ATT TCG AAA AAG TTG GCC	4339	
904	L L N V I G R K I W K K L A	917	
4340	GAA ATA TTA GGA TAT ACG AGT AGG CGT TTC TTG TCC TCT GCA GAA GTC AAA TG gtcagctgct	4401	
918	E I L G Y T S R R F L S S A E V K W	935	
4402	ggtcttcgagacttcagcaatattgacacatcag G CTT TTT TGT CTT GGA ATG AGA GAT GGT TTG AAA	4468	
936	L F C L G M R D G L K	946	
4469	CCC TCT TTC AAA TAT CAT CCA TCC TTC GAA CAG CTA ATA TAC CAA TTT CAG TCA TTG ACT	4528	
947	P S F K Y H P C F E Q L I Y Q F Q E L T	966	
4529	GAT CTT ATC AAG CCC CTA AGA CCA GTT TTG CGA CAG GTG TTA TTT TTA CAT AGA AGA ATA	4588	
967	D L I K P L R P V L R Q V L F L H R R I	986	
4589	GCT GAT TAA cgtcattctcttaacttattatatacatatctcttactctggtctctcttaacaatactattacttaagcata	4665	
987	A D	989	

# Figure 15

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4666 gctgacccccaaagcaagcatatcaggacccccagcaaaagcaaaatcaacccgctcattcgtcttcgactgacttcgtcc 4745  
4746 cttatcccttatccttttaagaaaagattgacagctggcttgcctgactcctgcccacatgcccattcaaacgggagctggctaaaca 4825  
4826 ttaaaagtaatacatgaggctaatctctctctcattcagaaacaggaaaagctggctctctataatgaataaatgcccgcacca 4905  
4906 atgczaaaagacgaagattatctcttaaaccaagggggactcagcatatccgaaaggzaaaagagagcaatcataccctagctgtc 4985  
4986 gctgaagaaaagcaaggataaatttcggaacaagctctctgcagatgacagggctaaatctctggctgacctgactctctggtaaaagc 5065  
5066 cccaggttatccatggtggccggcccttgcctactgagacgaaaagaaactcaggacagctctgaaactaatagctcattca 5145  
5146 atgtcttatataaggtctctctctctctgacctcactctctgcatgggtgaaaaaagaaatagctgcttaagccattatcgga 5225  
5225 cccgaaatagccaaactctctctggctctctcaaaagcggaaagctctaaagaactctctgaaagctctcagggctctcaaaactcc 5305  
5306 ccttgatttaaaaggaggaaatctctcaccgatcaggaaaatcggaatagctctacccgctctctgaggagaaagctctaatctctgc 5385  
5386 aaaaaaagaaaatctcatttgggagacatctctctgactgaacagatcgaggagagctctctccagcggatctcttgatgtcaata 5465  
5466 acctctatctctgaaatgcatggctctctacccgctctctgactctctctgagctctctccagctctagctgacctaaaggtacc 5544

66207T ED52E460

FIGURE 16  
\_page 1  
(Seq. ID. No. 1)

1 gcagcgctgc gtcctgctgc gcacgtggga agccctggcc ccggccaccc ccgcgatgcc  
61 gcgcgctccc cgtgcccag cctgctgcgc agccactacc gcgaggtgct  
121 gccgctggcc acgttcgtgc ggcgcctggg gcccagggc tggcggctgg tcgagcgcg  
181 ggacccggcg gctttccgcg cgtcgtggc ccagtgctg gtgtgcgtgc cctgggacgc  
241 acggccgccc cccgcccgc cctccttccg ccaggtgtcc tgctgaagg agctggtggc  
301 ccgagtgctg cagaggctgt gcgagcgcg cggaagaac gtgctggcct tcggcttcgc  
361 gctgctggac ggggcccgc ggggcccccc cgaggccttc accaccagcg tgcgcagcta  
421 cctgcccaac acggtgaccg acgcactgcg ggggagcggg gcgtgggggc tgctgctgcg  
481 ccgcgtgggc gacgacgtgc tggttcacct gctggcacgc tgcgcgctct ttgtgctggt  
541 ggctcccagc tgcgcctacc aggtgtgcgg gccgcgctg taccagctcg gcgctgccac  
601 tcaggccccg ccccgccac acgctagtgg accccgaagg cgtctgggat gcgaacgggc  
661 ctggaaccat agcgtcaggg aggcgggggt cccctgggc ctgccagccc cgggtgcgag  
721 gaggcgcggg ggcagtgcga gccgaagtct gccgttgccc aagaggccca ggcgtggcgc  
781 tgccccctgag ccggagcgga cgcctgttg gcaggggtcc tgggcccacc cgggcaggac  
841 gcgtggaccg agtgaccgtg gtttctgtgt ggtgtcacct gccagaccgc ccgaagaagc  
901 cacctctttg gaggggtgcg tctctggcac gcgccactcc caccatccg tgggcccga  
961 gcaccacgcg ggcctcccat ccacatcgcg gccaccacgt ccctgggaca cgccttgtcc  
1021 cccggtgtac gccgagacca agcacttcct ctactcctca ggcgacaagg agcagctgcg  
1081 gccctccttc ctactcagct ctctgaggcc cagcctgact ggcgctcgga ggctcgtgga  
1141 gaccatcttt ctgggttcca ggcctggat gccagggact ccccgaggt tgcctccct  
1201 gccccagcgc tactggcaaa tgcggccct gtttctggag ctgcttggga accacgcgca  
1261 gtgccccctac ggggtgctcc tcaagacgca ctgcccgctg cgagctgcgg tcacccagc  
1321 agccggtgtc tgtgcccggg agaagcccca gggctctgtg gcggcccccg aggaggagga  
1381 cacagacccc cgtgcctggg tgcagctgct ccgccagcac agcagccccc ggcaggtgta  
1441 cggcttctgt cgggcccgc tgcgcggct ggtgccccca ggctctggg gctccaggca  
1501 caacgaacgc cgttccctca ggaacaccaa gaagtcatc tccctgggga agcatgccaa  
1561 gctctcgtg caggagctga cgtggaagat gagcgtgcgg gactgcgctt gctgcgcag  
1621 gaccccaggg gttggctgtg ttccggccgc agagcaccgt ctgctgagg agatcctggc  
1681 caagtctctg cactggctga tgagtgtgta cgtcgtcgag ctgctcaggt ctttcttcta  
1741 tgtcacggag accacgttcc aaaagaacag gctcttttcc taccggaaga gtgtctggag  
1801 caagtgtcaa agcattggaa tcagacagca cttgaagagg gtgcagctgc gggagctgtc  
1861 ggaagcagag gtcaggcagc atcgggaagc caggcccgc ctgctgacgt ccagactccg  
1921 cttcatcccc aagcctgacg ggctgcggcc gattgtgaac atggactacg tcgtgggagc  
1981 cagaacgttc cgcagagaaa agagggccga gcgtctcacc tcgaggggtga aggcactgtt  
2041 cagcgtgctc aactacgagc gggcgcgcg ccccgccctc ctgggcgctt ctgtgctggg  
2101 cctggacgat atccacaggg cctggcgcac cttcgtgctg cgtgtgcggg cccaggaccc  
2161 gccgcctgag ctgtactttg tcaaggtgga tgtgacgggc gcgtacgaca ccatccccca  
2221 ggacaggctc acggaggtca tcgccagcat catcaaacc cagaacacgt actgcgtgcg  
2281 tcggtatgcc gtggtccaga aggcgcgcca tgggcacgtc cgcaaggcct tcaagagcca  
2341 cgtctctacc ttgacagacc tccagccgta catgcgacag ttcgtggctc acctgcagga  
2401 gaccagcccg ctgagggatg ccgtcgtcat cgagcagagc tcctccctga atgaggccag  
2461 cagtggcctc ttcgacgtct tcctacgctt catgtgccac cacgccgtgc gcacagggg  
2521 caagtccctac gtccagtgc aggggatccc gcagggtcc atcctctcca cgtgctctg  
2581 cagcctgtgc tacggcgaca tggagaacaa gctgtttgcg gggattcggc gggacgggct  
2641 gctcctgctg ttggtggatg atttcttgtt ggtgacacct cacctaccc acgcgaaaac  
2701 cttcctcagg accctggctc gaggtgtccc tgagtatggc tgcgtgggtga acttgcggaa  
2761 gacagtgggtg aacttccctg tagaagacga ggcctgggtt ggcacggctt ttgttcagat  
2821 gccggccccc ggcctattcc cctgggtgcg cctgctgctg gatacccgga ccttggaggt  
2881 gcagagcgac tactccagct atgcccggac ctccatcaga gccagtctca ctttcaaccg

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FIGURE 16  
page 2  
(Seq. ID. No. 1)

2941 cggcttcaag gctgggagga acatgcgtcg caaactcttt ggggtcttgc ggctgaagtg  
3001 tcacagcctg tttctggatt tgcaggtgaa cagcctccag acggtgtgca ccaacatcta  
3061 caagatcctc ctgctgcagg cgtacaggtt tcacgcatgt gtgctgcagc tcccatttca  
3121 tcagcaagtt tggagaagacc ccacattttt cctgcgcgtc atctctgaca cggcctccct  
3181 ctgctactcc atcctgaaag ccaagaacgc agggatgtcg ctggggggcca agggcgccgc  
3241 cggccctctg cctccgagg ccgtgcagtg gctgtgccac caagcattcc tgctcaagct  
3301 gactcgacac cgtgtcacct acgtgccact cctgggggtca ctcaggacag cccagacgca  
3361 gctgagtcgg aagctcccgg ggacgacgct gactgccctg gaggccgcag ccaaccgggc  
3421 actgccctca gacttcaaga ccaccttggga ctgatggcca cccgcccaca gccaggccga  
3481 gagcagacac cagcagccct gtcacgccgg gctctacgtc ccagggaggg agggcgccgc  
3541 cacaccaggg cccgcaccgc tgggagtcct aggcctgagt gagtgtttgg ccgaggcctg  
3601 catgtccggc tgaaggctga gtgtccggct gaggcctgag cgagtgtcca gccaaaggct  
3661 gagtgtccag cacacctgcc gtcttcactt cccacaggc tggcgctcgg ctccaccca  
3721 gggccagctt ttctcacca ggagcccggc ttccactccc cacataggaa tagtccatcc  
3781 ccagattcgc cattgttcac cctcgccct gccctccttt gccttccacc cccaccatcc  
3841 aggtggagac cctgagaagg accctgggag ctctgggaat ttggagtga caaagggtgtg  
3901 cctgtacac aggcgaggac cctgcacctg gatgggggtc cctgtgggtc aaattggggg  
3961 gaggtgctgt gggagtaaaa tactgaatat atgagttttt cagttttgaa aaaaa

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FIGURE 17  
HUMAN TRT PROTEIN SEQUENCE  
(SEQ. NO. 2)

MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDP  
AAFRALVAQCLVCVPWDARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFA  
LLDGARGGPPPEAFTTSVRSYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFV  
LVAPSCAYQVCGPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPA  
PGARRRGGSASRSLPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPA  
RPAEEATSLEGALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYS  
SGDKEQLRPSFLLSSLRPSLTGARRLVETIFLGSRPWMPGTFRRLPRLPQRYWQMRPL  
FLELLGNHAQCPYGVLLKTHCPLRAAVTPAAGVCAREKPGQSVAAPEEEDTDPRRLVQ  
LLRQHSSPWQVYGFVRACLRLRVPPGLWGSRHNERFLRNTKKFISLGKHAKLSLQEL  
TWKMSVRDCAWLRRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTET  
TFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFI  
PKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLG  
LDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYC  
VRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHLQETSPLRDAVVIEQSSSL  
NEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPOGSILSTLLCSLCYGD MENKLFAG  
IRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEAL  
GGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTFNRGFKAGRNMRR  
KLFGVLRLLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLPFHQQVWKNPT  
FFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLCLKLTRHRVT  
YVPLLGSRLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD

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FIGURE 18  
Clone 712562  
(SEQ ID NO. 3)

GGCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTT  
TTATGTCACGGAGACCACGTTTCAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTG  
GAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGACAGCTGCGGGAGCT  
GTCGGAAGCAGAGGTGAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACT  
CCGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGG  
AGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACT  
GTTCAGCGTGCTCAACTACGAGCGGGCGCGGCCCGCCCTCCTGGGCGCCTCTGTGCT  
GGGCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCAGGA  
CCCGCCGCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCC  
CCAGGACAGGCTCACGGAGGTATCGCCAGCATCATCAAACCCAGAACACGTAAGCGT  
GCGTCGGTATGCCGTGGTCCAGAAGGCCGCCATGGGCACGTCCGCAAGGCCTTCAAGAG  
CCACGTCCTACGTCCAGTCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCT  
GCAGCCTGTGCTACGGCGACATGGAGAACAAAGCTGTTTGCGGGGATTTCGGCGGGACGGGC  
TGCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAA  
CCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAAGTTCGCGA  
AGACAGTGGTGAAGTTCCTGTAGAACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGA  
TGCCGGCCCCACGGCCTATTTCCCTGGTGCAGCCTGCTGCTGGATAACCGGACCCTGGAGG  
TGCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACC  
GCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACCTTTTGGGGTCTTGCGGCTGAAGT  
GTCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCT  
ACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTT  
ATCAGCAAGTTTGAAGAACCCACATTTTTCTGCGCGTCATCTCTGACACGGCCTCCC  
TCTGCTACTCCATCCTGAAAGCCAAGAACGAGGATGTGCTGGGGGCCAAGGGCGCCG  
CCGGCC7TCTGCCCTCCGAGGCGGTGCAGTGGCTGTGCCACCAAGCATTCTGCTCAAGC  
TGACTCGACACCGTGTACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACGC  
AGCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGACCCAACCCGG  
CACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCACAGCCAGGCCG  
AGAGCAGACACCAGCAGCCCTGTACGCCGGGCTCTACGTCCAGGGAGGGAGGGGCGGC  
CCACACCCAGGCCTGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTGTTGGCCGAGGCCT  
GCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGC  
TGAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCC  
AGGGCCAGCTTTTCTCACCAGGAGCCCGGCTTCACTCCCCACATAGGAATAGTCCATC  
CCCAGATTCGCCATTGTTACCCCTCGCCCTGCCCTCCTTTGCCTTCCACCCCCACCATC  
CAGGTGGAGACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGT  
GCCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGG  
GGAGGTGCTGTGGGAGTAAATACTGAATATATGAGTTTTTTCAGTTTTTG0AAAAAAAAA  
AAAAAAAAAAAAAAAAA

6520T 603460

FIGURE 19-

SEQ ID NO. 10

MetSerValTyrValValGluLeuLeuArgSerPhePhe  
TyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTrp  
SerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGluLeu  
SerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArgLeu  
ArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValValGly  
AlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAlaLeu  
PheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerValLeu  
GlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGlnAsp  
ProProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIlePro  
GlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCysVal  
ArgArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLysSer  
HisValLeuArgProValProGlyAspProAlaGlyLeuHisProLeuHisAlaAlaLeu  
GlnProValLeuArgArgHisGlyGluGlnAlaValCysGlyAspSerAlaGlyArgAla  
AlaProAlaPheGlyGly

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# FIGURE 20

Page 1

## SEQUENCE NO. 4 (DNA) AND SEQUENCE NO. 5 (PROTEIN) (TRANSLATION OF A $\Delta$ 182 hTRT VARIANT)

1  
met  
GCAGCGCTGCGTCCTGCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCG ATG

10  
pro arg ala pro arg cys arg ala val arg ser leu leu arg ser  
CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC

20 30  
his tyr arg glu val leu pro leu ala thr phe val arg arg leu  
CAC TAC CGC GAG GTG CTG CCG CTG GCC ACG TTC GTG CGG CGC CTG

40  
gly pro gln gly trp arg leu val gln arg gly asp pro ala ala  
GGG CCC CAG GGC TGG CGG CTG GTG CAG CGC CCG GAC CCG GCG GCT

50 60  
phe arg ala leu val ala gln cys leu val cys val pro trp asp  
TTC CGC GCG CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC

70  
ala arg pro pro pro ala ala pro ser phe arg gln val ser cys  
GCA CGG CCG CCC CCC GCC GCC CCC TCC TTC CGC CAG GTG TCC TGC

80 90  
leu lys glu leu val ala arg val leu gln arg leu cys glu arg  
CTG AAG GAG CTG GTG GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC

100  
gly ala lys asn val leu ala phe gly phe ala leu leu asp gly  
GGC GCG AAG AAC GTG CTG GCC TTC GGC TTC GCG CTG CTG GAC GGG

110 120  
ala arg gly gly pro pro glu ala phe thr thr ser val arg ser  
GCC CGC GGG GGC CCC CCC GAG GCC TTC ACC ACC AGC GTG CGC AGC

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# FIGURE 20

Page 2

130  
tyr leu pro asn thr val thr asp ala leu arg gly ser gly ala  
TAC CTG CCC AAC ACG GTG ACC GAC GCA CTG CGG GGG AGC GGG GCG

140 150  
trp gly leu leu leu arg arg val gly asp asp val leu val his  
TGG GGG CTG CTG CTG CGC CGC GTG GGC GAC GAC GTG CTG GTT CAC

160  
leu leu ala arg cys ala leu phe val leu val ala pro ser cys  
CTG CTG GCA CGC TGC GCG CTC TTT GTG CTG GTG GCT CCC AGC TGC

170 180  
ala tyr gln val cys gly pro pro leu tyr gln leu gly ala ala  
GCC TAC CAG GTG TGC GGG CCG CCG CTG TAC CAG CTC GGC GCT GCC

190  
thr gln ala arg pro pro pro his ala ser gly pro arg arg arg  
ACT CAG GCC CGG CCC CCG CCA CAC GCT AGT GGA CCC CGA AGG CGT

200 210  
leu gly cys glu arg ala trp asn his ser val arg glu ala gly  
CTG GGA TGC GAA CGG GCC TGG AAC CAT AGC GTC AGG GAG GCC GGG

220  
val pro leu gly leu pro ala pro gly ala arg arg arg gly gly  
GTC CCC CTG GGC CTG CCA GCC CCG GGT GCG AGG AGG CGC GGG GGC

230 240  
ser ala ser arg ser leu pro leu pro lys arg pro arg arg gly  
AGT GCC AGC CGA AGT CTG CCG TTG CCC AAG AGG CCC AGG CGT GGC

250  
ala ala pro glu pro glu arg thr pro val gly gln gly ser trp  
GCT GCC CCT GAG CCG GAG CGG ACG CCC GTT GGG CAG GGG TCC TGG

260 270  
ala his pro gly arg thr arg gly pro ser asp arg gly phe cys  
GCC CAC CCG GGC AGG ACG CGT GGA CCG AGT GAC CGT GGT TTC TGT

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# FIGURE 20

Page 3

280  
val val ser pro ala arg pro ala glu glu ala thr ser leu glu  
GTG GTG TCA CCT GCC AGA CCC GCC GAA GAA GCC ACC TCT TTG GAG

290 300  
gly ala leu ser gly thr arg his ser his pro ser val gly arg  
GGT GCG CTC TCT GGC ACG CGC CAC TCC CAC CCA TCC GTG GGC CGC

310  
gln his his ala gly pro pro ser thr ser arg pro pro arg pro  
CAG CAC CAC GCG GGC CCC CCA TCC ACA TCG CGG CCA CCA CGT CCC

320 330  
trp asp thr pro cys pro pro val tyr ala glu thr lys his phe  
TGG GAC ACG CCT TGT CCC CCG GTG TAC GCC GAG ACC AAG CAC TTC

340  
leu tyr ser ser gly asp lys glu gln leu arg pro ser phe leu  
CTC TAC TCC TCA GGC GAC AAG GAG CAG CTG CGG CCC TCC TTC CTA

350 360  
leu ser ser leu arg pro ser leu thr gly ala arg arg leu val  
CTC AGC TCT CTG AGG CCC AGC CTG ACT GGC GCT CGG AGG CTC GTG

370  
glu thr ile phe leu gly ser arg pro trp met pro gly thr pro  
GAG ACC ATC TTT CTG GGT TCC AGG CCC TGG ATG CCA GGG ACT CCC

380 390  
~~arg arg leu pro arg leu pro gln arg tyr trp gln met arg pro~~  
~~CGC AGG TTG CCC CGC CTG CCC CAG CGC TAC TGG CAA ATG CGG CCC~~

400  
leu phe leu glu leu leu gly asn his ala gln cys pro tyr gly  
CTG TTT CTG GAG CTG CTT GGG AAC CAC GCG CAG TGC CCC TAC GGG

410 420  
val leu leu lys thr his cys pro leu arg ala ala val thr pro  
GTG CTC CTC AAG ACG CAC TGC CCG CTG CGA GCT GCG GTC ACC CCA

430

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# FIGURE 20

Page 4

ala ala gly val cys ala arg glu lys pro gln gly ser val ala  
GCA GCC GGT GTC TGT GCC CGG GAG AAG CCC CAG GGC TCT GTG GCG

440

ala pro glu glu glu asp thr asp pro arg arg leu val gln leu  
GCC CCC GAG GAG GAG GAC ACA GAC CCC CGT CGC CTG GTG CAG CTG

450

460

leu arg gln his ser ser pro trp gln val tyr gly phe val arg  
CTC CGC CAG CAC AGC AGC CCC TGG CAG GTG TAC GGC TTC GTG CGG

470

ala cys leu arg arg leu val pro pro gly leu trp gly ser arg  
GCC TGC CTG CGC CGG CTG GTG CCC CCA GGC CTC TGG GGC TCC AGG

480

490

his asn glu arg arg phe leu arg asn thr lys lys phe ile ser  
CAC AAC GAA CGC CGC TTC CTC AGG AAC ACC AAG AAG TTC ATC TCC

500

leu gly lys his ala lys leu ser leu gln glu leu thr trp lys  
CTG GGG AAG CAT GCC AAG CTC TCG CTG CAG GAG CTG ACG TGG AAG

510

520

met ser val arg asp cys ala trp leu arg arg ser pro gly val  
ATG AGC GTG CGG GAC TGC GCT TGG CTG CGC AGG AGC CCA GGG GTT

530

gly cys val pro ala ala glu his arg leu arg glu glu ile leu  
GGC TGT GTT CCG GCC GCA GAG CAC CGT CTG CGT GAG GAG ATC CTG

540

550

ala lys phe leu his trp leu met ser val tyr val val glu leu  
GCC AAG TTC CTG CAC TGG CTG ATG AGT GTG TAC GTC GTC GAG CTG

560

leu arg ser phe phe tyr val thr glu thr thr phe gln lys asn  
CTC AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC

570

580

arg leu phe phe tyr arg lys ser val trp ser lys leu gln ser  
AGG CTC TTT TTC TAC CGG AAG AGT GTC TGG AGC AAG TTG CAA AGC

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# FIGURE 20

Page 5

590 600  
ile gly ile arg gin his leu lys arg val gln leu arg glu leu  
ATT GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG

610  
ser glu ala glu val arg gln his arg glu ala arg pro ala leu  
TCG GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG

620 630  
leu thr ser arg leu arg phe ile pro lys pro asp gly leu arg  
CTG ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG

640  
pro ile val asn met asp tyr val val gly ala arg thr phe arg  
CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC

650 660  
arg glu lys arg ala glu arg leu thr ser arg val lys ala leu  
AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG

670  
phe ser val leu asn tyr glu arg ala arg arg pro gly leu leu  
TC AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC GGC CTC CTG

680 690  
gly ala ser val leu gly leu asp asp ile his arg ala trp arg  
GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC

700  
thr phe val leu arg val arg ala gln asp pro pro pro glu leu  
ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG CTG

710 720  
tyr phe val lys val asp val thr gly ala tyr asp thr ile pro  
TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC

730  
gln asp arg leu thr glu val ile ala ser ile ile lys pro gln  
CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG

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## Page 6

his gly his val arg lys ala phe lys ser his val leu arg pro  
CAT GGG CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC CTA CGT CCA

770											780				
val	pro	gly	asp	pro	ala	gly	leu	his	pro	leu	his	ala	ala	leu	
GTG	CCA	GGG	GAT	CCC	GCA	GGG	CTC	CAT	CCT	CTC	CAC	GCT	GCT	CTG	

790  
gln pro val leu arg arg his gly gln ala val cys gly asp  
CAG CCT GTG CTA CGG CGA CAT GGA GAA CAA GCT GTT TGC GGG GAT

800 807

ser ala gly arg ala ala pro ala phe gly gly OP

TCG GCG GGA CGG GCT GCT CCT GCG TTT GGT GGA TGA TTTCTTGTGGT

GACACCTCACCTCACCCACGCGAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGA  
GTATGGCTGCGTGGTGAACCTTGCGGAAGACAGTGGTGAACCTTCCTGTAGAAGACGAGGC  
CCTGGGTGGCACGGCTTTTGTTCAGATGCCGGCCACGGCCTATTCCCCTGGTGCGGCCT  
GCTGCTGGATACCCGGACCCTGGAGGTGCAGAGCGACTACTCCAGCTATGCCCGGACCTC  
CATCAGAGCCAGTCTCACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGA  
ACTCTTTGGGGTCTCCTCAGGACCCTGGTCCGAGGTGTCCCTGA

CCTCCAGACGGTGTGCACCAACATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCA  
CGCATGTGTGCTGCAGCTCCCATTTTCATCAGCAAGTTTGGAAGAACCCACATTTTTCT  
GCGCGTCATCTCTGACACGGCCTCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGG  
GATGTCGCTGGGGGCCAAGGGCGCCGCCGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCT  
GTGCCACCAAGCATTTCCTGCTCAAGCTGACTCGACACCGTGTACCTACGTGCCACTCCT

# FIGURE 20

Page 7

GGGGTCACTCAGGACAGCCCAGACGCAGCTGAGTCGGAAGCTCCCGGGGACGACGCTGAC  
TGCCCTGGAGGCCGCGAGCCAACCCGGCACTGCCCTCAGACTTCAAGACCATCCTGGACTG  
ATGGCCACCCGCCCACAGCCAGGCCGAGAGCAGACACCAGCAGCCCTGTACGCCGGGCT  
CTACGTCCCAGGGAGGGAGGGGCGGCCACACCCAGGCCCGCACCGCTGGGAGTCTGAGG  
CCTGAGTGAGTGTTTGGCCGAGGCCTGCATGTCCGGCTGAAGGCTGAGTGTCGGCTGAG  
GCCTGAGCGAGTGTCAGCCAAGGGCTGAGTGTCAGCACACCTGCCGTCTTCACTTCCC  
CACAGGCTGGCGCTCGGCTCCACCCAGGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTC  
CACTCCCCACATAGGAATAGTCCATCCCCAGATTCGCCATTGTTCACCCCTCGCCCTGCC  
CTCCTTTGCCTTCCACCCCCACCATCCAGGTGGAGACCCTGAGAAGGACCCTGGGAGCTC  
TGGAATTGAGTGACCAAAGGTGTGCCCTGTACACAGGCGAGGACCCTGCACCTGGAT  
GGGGTCCCTGTGGGTCAAATTGGGGGGAGGTGCTGTGGGAGTAAAATACTGAATATATG  
AGTTTTTTCAGTTTTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 21-  
Genomic DNA insert of pGRN144

Seq. ID. No. 6

1 CCATGGGACCCACTGCAGGGGCAGCTGGGAGGCTGCAGGCTTCAGGTCCCAGTGGGGTTG  
GGTACCCTGGGTGACGTCCCCGTCGACCCTCCGACGTCCGAAGTCCAGGGTCACCCCAAC  
61 CCATCTGCCAGTAGAAACCTGATGTAGAATCAGGGCGCGAGTGTGGACACTGTCCTGAAT  
GGTAGACGGTCATCTTTGGACTACATCTTAGTCCCGCGCTCACACCTGTGACAGGACTTA  
121 CTCAATGTCTCAGTGTGTGCTGAAACATGTAGAAATTAAAGTCCATCCCTCCTACTCTAC  
GAGTTACAGAGTCACACACGACTTTGTACATCTTTAATTTTCAGGTAGGGAGGATGAGATG  
181 TGGGATTGAGCCCCCTTCCCTATCCCCCCCCAGGGGCAGAGGAGTTCCTCTCACTCCTGTG  
ACCCTAACTCGGGGAAGGGATAGGGGGGGGTCCCCGTCTCCTCAAGGAGAGTGAGGACAC  
241 GAGGAAGGAATGATACTTTGTTATTTTTCACTGCTGGTACTGAATCCACTGTTTCATTTG  
CTCCTTCCTTACTATGAAACAATAAAAAGTGACGACCATGACTTAGGTGACAAAGTAAAC

\*\*\*\*\*  
301 TTGGTTTGTGTTTGTGTTTGTGTTTGTGAGAGGCGGTTTCACTCTTGTGCTCAGGCTGGAGGGAG  
AACCAAACAAACAAACAAACAACTCTCCGCCAAAGTGAGAACAACGAGTCCGACCTCCCTC

\*\*\*\*\*  
361 TGCAATGGCGCGATCTTGGCTTACTGCAGCCTCTGCCTCCCAGGTTCAAGTGATTCTCCT  
ACGTTACCGCGCTAGAACCGAATGACGTCCGAGACGGAGGGTCCAAGTTCACTAAGAGGA

alu  
\*\*\*\*\*  
421 GCTTCCGCCTCCCATTTGGCTGGGATTACAGGCACCCGCCACCATGCCAGCTAATTTTT  
CGAAGGCGGAGGGTAAACCGACCCTAATGTCCGTGGGCGGTGGTACGGGTGATTAAAAA

==  
\*\*\*\*\*  
481 TGTATTTTGTAGTAGAGACGGGGGTGGGGGTGGGGTTCACCATGTTGGCCAGGCTGGTCTC  
ACATAAAAATCATCTCTGCCCCACCCCCACCCAAGTGGTACAACCGGTCCGACCAGAG

CAP  
===== >  
\*\*\*\*\*  
1 541 GAACTTCTGACCTCAGATGATCCACCTGCCTCTGCCTCCTAAAGTGCTGGGATTACAGGT  
CTTGAAGACTGGAGTCTACTAGGTGGACGGAGACGGAGGATTTACGACCCTAATGTCCA

\*\*\*\*\*  
601 GTGAGCCACCATGCCAGCTCAGAATTTACTCTGTTTAGAAACATCTGGGTCTGAGGTAG  
CACTCGGTGGTACGGGTGAGTCTTAAATGAGACAAATCTTTGTAGACCCAGACTCCATC

66207T-EGGEGH60

FIGURE 21 (continued, 2 of 6)

CCAAT

\*\*\*\*\*>

661 GAAGCTCACCCCACTCAAGTGTGTTGGTGTGTTTAAGCCAATGATAGAATTTTTTTTATTGT  
CTTCGAGTGGGGTGAGTTCACAACACCACAAAATTCGGTTACTATCTTAAAAAATAACA

721 TGTTAGAACACTCTTGATGTTTTACACTGTGATGACTAAGACATCATCAGCTTTTCAAAG  
ACAATCTTGTGAGAACTACAAAATGTGACACTACTGATTCTGTAGTAGTCGAAAAGTTTC

CAP

\*\*\*\*\*>

781 ACACACTAACTGCACCCATAATACTGGGGTGTCTTCTGGGTATCAGCGATCTTCATTGAA  
TGTGTGATTGACGTGGGTATTATGACCCACAGAAGACCCATAGTCGCTAGAAGTAACCT

CAP

\*\*\*\*\*>

841 TGCCGGGAGGCGTTTCCTCGCCATGCACATGGTGTAAATTACTCCAGCATAATCTTCTGC  
ACGGCCCTCCGCAAAGGAGCGGTACGTGTACCACAATTAATGAGGTCGTATTAGAAGACG

\*\*\*>

901 TTCCATTCTTCTCTTCCCTCTTTTAAAATTGTGTTTTCTATGTTGGCTTCTCTGCAGAG  
AAGGTAAAGAAGAGAAGGGAGAAAATTTTAACACAAAAGATACAACCGAAGAGACGTCTC

CAP

\*\*\*\*\*>

961 AACCAGTGTAAGCTACAACCTAACTTTTGTGGAACAAATTTTCAAACCGCCCTTTGC  
TTGGTCACATTCGATGTTGAATTGAAAACAACCTTGTTTAAAAGGTTTGGCGGGGAAACG

1021 CCTAGTGGCAGAGACAATTACAAACACAGCCCTTTAAAAGGCTTAGGGATCACTAAGG  
GGATCACCGTCTCTGTTAAGTGTTTGTGTCGGGAAATTTTCCGAATCCCTAGTGATTCC

1081 GGATTTCTAGAAGAGCGACCCGTAATCCTTAAGTATTTACAAGACGAGGCTAACCTCCAG  
CCTAAAGATCTTCTCGCTGGGCATTAGGAATTCATAAATGTTCTGCTCCGATTGGAGGTC

1141 CGAGCGTGACAGCCAGGGAGGGTGCGAGGCCTGTTCAAATGCTAAGCTTCCATAAATAA  
GCTCGCACTGTCCGGTCCCTCCACGCTCCGGACAAGTTTACGATTGGAAGGTATTTATT

1201 AGCAAATTTCTCCGGCAGTTTCTGGAAAGTAGGAAAGGTTAACATTTAAGGTTGCGTTT  
TCGTTTAAAGGAGGCCGTCAAAGACCTTTCATCCTTTCCAATTGTAAATTCCAACGCAAA

1261 GTTAGCATTTCAAGTGTGTTGCCGACCTCAGCTAACAGCATCCCTGCAAGGCCTCGGGAGAC  
CAATCGTAAAGTCACAAACGGCTGGAGTCGATTGTCGTAGGGACGTTCCGGAGCCCTCTG

1321 CCAGAAGTTTCTCGCCCTTAGATCCAACTTGAGCAACCCGGAGTCTGGATTCTTGGA  
GGTCTTCAAAGAGCGGGGAATCTAGGTTTGAACCTCGTTGGGCCTCAGACCTAAGGACCCT

TopoII

\*\*\*\*\*>

1381 AGTCCTCAGCTGTCCTGCGGTTGTGCCGGGGCCCCAGGTCTGGAGGGGACCAGTGGCCGT  
TCAGGAGTCGACAGGACGCCAACACGGCCCCGGGGTCCAGACCTCCCCTGGTCACCGGCA

1441 GTGGCTTCTACTGCTGGGCTGGAAGTCGGGCCTCCTAGCTCTGCAGTCCGAGGCTTGGA  
CACCGAAGATGACGACCCGACCTTCAGCCCGGAGGATCGAGACGTCAGGCTCCGAACCTC

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FIGURE 21 (continued, 3 of 6)

1501 CCAGGTGCCTGGACCCCGAGGCTGCCCTCCACCCTGTGCGGGCGGGATGTGACCAGATGT  
GGTCCACGGACCTGGGGCTCCGACGGGAGGTGGGACACGCCC GCCCTACACTGGTCTACA

1561 TGGCCTCATCTGCCAGACAGAGTGCCGGGGCCCAGGGTCAAGGCCGTTGTGGCTGGTGTG  
ACCGGAGTAGACGGTCTGTCTCACGGCCCCGGGTCCAGTTCGGGCAACACCGACCACAC

1621 AGGCGCCCCGGTGC GCGGCCAGCAGGAGCGCCTGGCTCCATTTCCACCCCTTCTCGACGG  
TCCGCGGGCCACGCGCCGGTCGTCTCGCGGACCGAGGTAAAGGGTGGGAAAGAGCTGCC

1681 GACCGCCCCGGTGGGTGATTAACAGATATTGGGGTGGTTTGCTCATGGTGGGGACCCCTT  
CTGGCGGGGCCACCCACTAATTGTCTATAACCCACCAAACGAGTACCACCCCTGGGGAA

1741 CGCCGCCTGAGAACCTGCAAAGAGAAATGACGGGCCTGTGTCAAGGAGCCCAAGTCGCGG  
GCGGCGGACTCTTGGACGTTTCTCTTTACTGCCCGACACAGTTCCTCGGGTTCAGCGCC

1801 GGAAGTGTTCAGGGAGGCACTCCGGGAGGTCCCGCGTGCCCGTCCAGGGAGCAATGCGT  
CCTTCACAACGTCCCTCCGTGAGGCCCTCCAGGGCGCACGGGCAGGTCCCTCGTTACGCA

1861 CCTCGGGTTCGTCCCCAGCCGCGTCTACGCGCCTCCGTCTCCCTTCACGTCCGGCATT  
GGAGCCCAAGCAGGGGTCCGCGCAGATGCGCGGAGGCAGGAGGGGAAGTGCAGGCCGTAA

1921 CGTGGTGC GCGGAGCCCGACGCCCCGCGTCCGGACCTGGAGGCAGCCCTGGGTCTCCGGA  
GCACCACGGGCCTCGGGCTGCGGGGCGCAGGCCTGGACCTCCGTGCGGACCCAGAGGCCT

1981 TCAGGCCAGCGGCCAAAGGGTCGCCGCACGCACCTGTTCCAGGGCCTCCACATCATGGC  
AGTCCGGTCGCCGGTTTCCAGCGGCGTGC GTGGACAAGGGTCCCGGAGGTGTAGTACCG

2041 CCCTCCCTCGGGTTACCCACAGCCTAGGCCGATTTCGACCTCTCTCCGCTGGGGCCCTCG  
GGGAGGGAGCCCAATGGGGTGTCCGATCCGGCTAAGCTGGAGAGAGGCGACCCCGGGAGC

Sp1

\*\*\*\*\*

2101 CTGGCGTCCCTGCACCCTGGGAGCGCGAGCGGCGCGGGCGGGGAAGCGCGGCCAGAC  
GACCGCAGGGACGTGGGACCCTCGCGCTCGCCGCGCGCCCGCCCTTCGCGCCGGGTCTG

2161 CCCCGGGTCCGCCCCGAGCAGCTGCGCTGTGCGGGCCAGGCCGGGCTCCAGTGGATTCTG  
GGGGCCAGGCGGGCCTCGTCGACGCGACAGCCCCGGTCCGGCCCGAGGGTCACCTAAGC

2221 CGGGCAACAGACGCCCAGGACCGCGCTTCCCACGTGGCGGAGGGACTGGGGACCCGGGCA  
GCCC GTTGTCTGCGGGTCTTGGCGCGAAGGGTGCACCGCCTCCCTGACCCCTGGGCCCGT

Sp1

=====

E2F

\*\*\*\*\*

2281 CCGGTCCTGCCCCCTTCACCTTCCAGCTCCGCCTCGTCCGCGCGGAACCCCGCCCCGTCCC  
GGCCAGGACGGGGAAGTGGAAGGTGAGGCGGAGCAGGCGCGCCTTGGGGCGGGGCAGGG

2341 GAACCCCTCCCGGGTCCCCGGCCCCAGCCCCCTCCGGGCCATCCAGCCCGTCCCGTTCTC  
CTTGGAAGGGCCAGGGGCCGGGTGCGGGAAGGCCCGGTAGGGTGGGCGAGGGCAAGGA

09432507.140299

\_\_\_\_\_

=====

**NFKB**

```

hTERT5'
*****>
2461 GCACGTGGGAAGCCCTGGCCCCGGCCACCCCGCGATGCCGCGCGCTCCCGCTGCCGAG
    CGTGCACCCCTTCGGGACCGGGGCCGCTGGGGGCGCTACGGCGCGGAGGGGCGACGGCTC

2521 CCGTGCCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTTCGTGC
    GGCACGCGAGGGACGACGCGTGGTGGTATGGCGCTCCACGACGGCGACCGGTGCAAGCAG

```

★ ★ ★ ★ ★ ★ ★

2641 CGCTGGTGGCCCAAGTGCCTGGTGTGCGTGCCCTGGGACGCACGGCCGCCCCCGCGCCCC  
GCGACCACCGGGTCACGGACCACACGCACGGGACCCTGCGTGCCGGCGGGGGGCGGCGGG

**三、结论**

\*\*\*\*\*  
2701 CCTCCTTCCGCCAGGTGGGCTCCCGGGGTTCGGCTTCGGCTGGGGTTGAGGGCGGCCG  
GGAGGAAGGCGGTCCACCCGGAGGGGCCCCAGCCGCAGGCCGACCCCAACTCCCGCCGGC

• • • • •  
• • • • •

+++++

[illegible][illegible]

2761 GGGGGAAC CAGCGACATGCGGAGAGCAGCGCAGGCGACTCAGGGCGCTTCCCCCGCAGGT  
CCCCCTTGGTCGCTGTACGCCCTCTCGTCGCGTCCGCTGAGTCCCGCGAAGGGGGCGTCCA

• • • •

2821 GTCCTGCCTGAAGGAGCTGGTGGCCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAA  
CAGGACGGACTTCCTCGACCACCGGGCTCACGACGTCTCCGACACGCTCGCGCCGCGCTT

2881 GAACGTGCTGGCCTTCGGCTTCGCGCTGCTGGACGGGGCCCGGGGGCCCCCGAGGC  
CTTGACGACCGGAAGCCGAAGCGCGACGACCTGCCCGGGCGCCCCGGGGGGCTCCG

2941 CTTCAACCACCAGCGTGCGCAGCTACCTGCCAACACGGTGACCGACGCACTGCGGGGGAG  
GAAGTGGTGGTTCGCACGCGTCGATGGACGGGTTGTGCCACTGGCTGCGTGACGCCCCCTC

[illegible]

FIGURE 21 (continued, 5 of 6)

3001 CGGGGCGTGGGGGCTGCTGCTGCGCCGCGTGGGCGACGACGTGCTGGTTACCTGCTGGC  
GCCCCGACCCCCGACGACGACGCGGCGCACCCGCTGCTGCACGACCAAGTGGACGACCG

3061 ACGCTGCGCGCTCTTTGTGCTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCC  
TGCGACGCGCGAGAAACACGACCACCGAGGGTGCACGCGGATGGTCCACACGCCCCGGCGG

3121 GCTGTACCAGCTCGGCGCTGCCACTCAGGCCCGGCCCCCGCCACACGCTAGTGGACCCCG  
CGACATGGTCGAGCCGCGACGGTGAGTCCGGGCGGGGGCGGTGTGCGATCACCTGGGGC

3181 AAGGCGTCTGGGATGCGAACGGGCCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCT  
TTCCGCAGACCCTACGCTTGCCCGGACCTTGGTATCGCAGTCCCTCCGGCCCCAGGGGGA

3241 GGGCCTGCCAGCCCCGGGTGCGAGGAGGCGCGGGGGCAGTGCCAGCCGAAGTCTGCCGTT  
CCCGGACGGTCGGGGCCCCACGCTCCTCCGCGCCCCCGTCACGGTCGGCTTCAGACGGCAA

3301 GCCCAAGAGGCCCCAGGCGTGCGCTGCCCCCTGAGCCGGAGCGGACGCCCCGTTGGGCAGGG  
CGGGTTCTCCGGGTCCGCACCGCGACGGGGACTCGGCCTCGCCTGCGGGCAACCCGTCCC

3361 GTCCTGGGCCCCACCCGGGCAGGACGCGTGACCGAGTGACCGTGTTTCTGTGTGGTGTG  
CAGGACCCGGGTGGGCCCCGTCTCGGCACCTGGCTCACTGGCACCAAAGACACACCACAG

3421 ACCTGCCAGACCCGCCGAAGAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCA  
TGGACGGTCTGGGCGGCTTCTTCGGTGGAGAAACCTCCACGCGAGAGACCGTGCGCGGT

3481 CTCCCACCCATCCGTGGGCGGCCAGCACCCACGCGGGCCCCCATCCACATCGCGGCCACC  
GAGGGTGGGTAGGCACCCGCGGTCTGGTGCGCCCGGGGGTAGGTGTAGCGCCGTTGG

3541 ACGTCCCTGGGACACGCTTGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTC  
TGCAGGGACCTGTGCGGAACAGGGGGGCCACATGCGGCTCTGGTTCGTGAAGGAGATGAG

3601 CTCAGGCGACAAGGAGCAGCTGCGGCCCTCCTTCTACTCAGCTCTCTGAGGCCCAGCCT  
GAGTCCGCTGTTCTCGTCGACGCCGGGAGGAAGGATGAGTCGAGAGACTCCGGGTCCGA

3661 GACTGGCGCTCGGAGGCTCGTGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGG  
CTGACCGCGAGCCTCCGAGCACCTCTGGTAGAAAGACCCAAGGTCCGGGACCTACGGTCC

3721 GACTCCCCGCAGGTTGCCCCGCCTGCCCCAGCGCTACTGGCAAATGCGGCCCCGTGTTTCT  
CTGAGGGGCGTCCAACGGGGCGGACGGGGTTCGCGATGACCGTTTACGCCGGGGACAAAGA

3781 GGAGCTGCTTGGAACACGCGCAGTGGGGCTAGGGGGTGCTCCTCAAGACGCACTGCCC  
CCTCGACGAACCCTTGGTGCGCGTCACGGGGATGCCCCACGAGGAGTTCTGCGTGACGGG

3841 GCTGCGAGCTGCGGTACCCCCAGCAGCCGGTGTCTGTGCCCGGGAGAAGCCCCAGGGCTC  
CGACGCTCGACGCCAGTGGGGTCGTCCGGCCACAGACACGGGCCCTCTTCGGGGTCCCGAG

3901 TGTGGCGGCCCCGAGGAGGAGGACACAGACCCCCGTGCGCTGGTGCAGCTGCTCCGCCA  
ACACCGCCGGGGGCTCCTCCTCCTGTGTCTGGGGGCAGCGGACCACGTGACGAGGCGGT

3961 GCACAGCAGCCCCTGGCAGGTGTACGGCTTCGTGCGGGCCTGCCTGCGCCGGCTGGTGGC  
CGTGTGCTCGGGGACCGTCCACATGCCGAAGCACGCCCGGACGGACGCGGCCGACCACGG

4021 CCCAGGCCTCTGGGGCTCCAGGCACAACGAACGCGCTTCCTCAGGAACACCAAGAAGTT  
GGGTCCGGAGACCCGAGGTCCGTGTTGCTTGCGGCGAAGGAGTCCTTGTGGTTCTTCAA

094330 053346

FIGURE 21 (continued, 6 of 6)

4081 CATCTCCCTGGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGT  
GTAGAGGGACCCCTTCGTACGGTTCGAGAGCGACGTCCTCGACTGCACCTTCTACTCGCA

\*\*\*\*\*  
4141 GCGGGACTGCGCTTGGCTGCGCAGGAGCCCAGGTGAGGAGGTGGTGGCCGTCGAGGGCCC  
CGCCCTGACGCGAACCGACGCGTCCTCGGGTCCACTCCTCCACCACCGGCAGCTCCCGGG

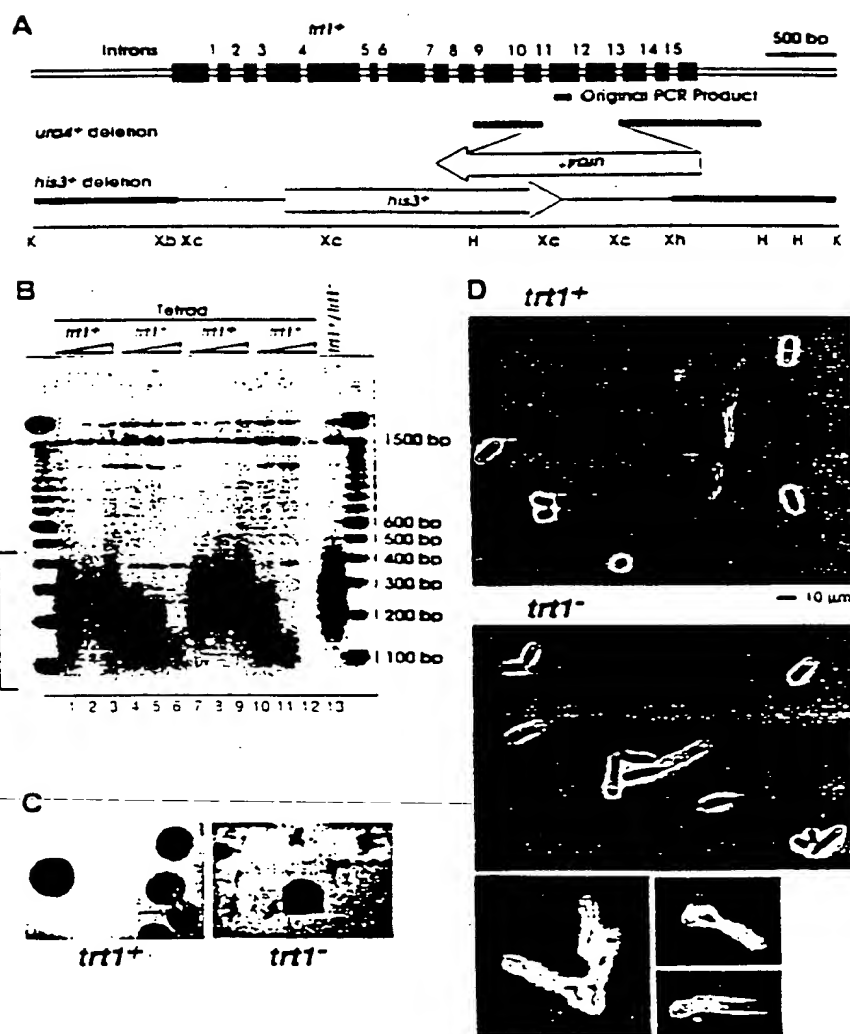
Intron2  
\*\*\*\*\*  
4201 AGGCCCCAGAGCTGAATGCAGTAGGGGCTCAGAAAAGGGGGCAGGCAGAGCCCTGGTCCT  
TCCGGGGTCTCGACTTACGTCATCCCCGAGTCTTTCCCCCGTCCGTCTCGGGACCAGGA

\*\*\*\*\*  
4261 CCTGTCTCCATCGTACAGTGGGCACACGTGGCTTTTCGCTCAGGACGTCGAGTGGACACG  
GGACAGAGGTAGCAGTGCACCCGTGTGCACCGAAAAGCGAGTCCTGCAGCTCACCTGTGC

\*\*\*\*\*>  
4321 GTGATCGAGGTCGAC  
CACTAGCTCCAGCTG

094950-1099  
66207-0053460

Figure 22



09433503 110299

FIGURE 23  
EST AA281296  
(Seq. ID. No. 8)

gc

caagttcctg cactgggtga tgagtgtgta cgtcgtcgag ctgctcaggt ctttctttta  
tgtcacggag accacgtttc aaaagaacag gctctttttc taccggaaga gtgtctggag  
caagttgcaa agcattggaa tcagacagca cttgaagagg gtgcagctgc gggacgtgtc  
ggaagcagag gtcaggcagc atcgggaagc caggcccgcc ctgctgacgt ccagactccg  
cttcattcccc aagcctgacg ggctgcgggc gattgtgaac atggactacg tcgtgggagc  
cagaacgttc cgcagagaaa agagggccga gcgtctcacc tcgaggggtga aggcactggt  
cagcgtgctc aactacgagc gggcgcg

0943303460

FIGURE 24 -  
(Seq. ID. No. 9)

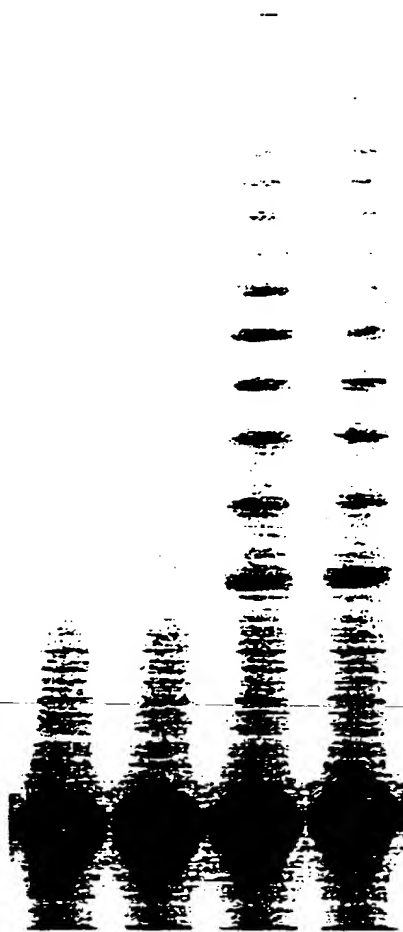
TCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAG  
ACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGC  
CAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCAT  
CAGGGGCAAGTC

09432503 110299

Figure 25

pBB5212

pGRN133



← Internal Control

Approximate Cell No.

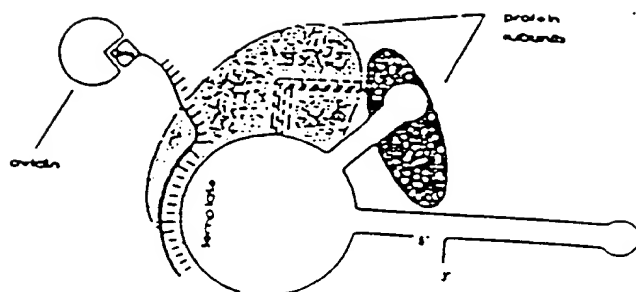
5,000 5,000 5,000 5,000

0943501109  
0620T' 0523E460



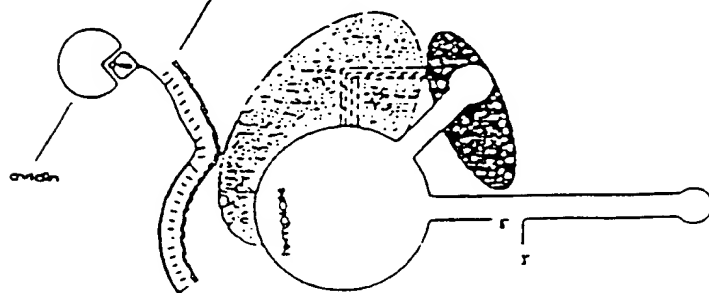
Figure 26

PANEL A



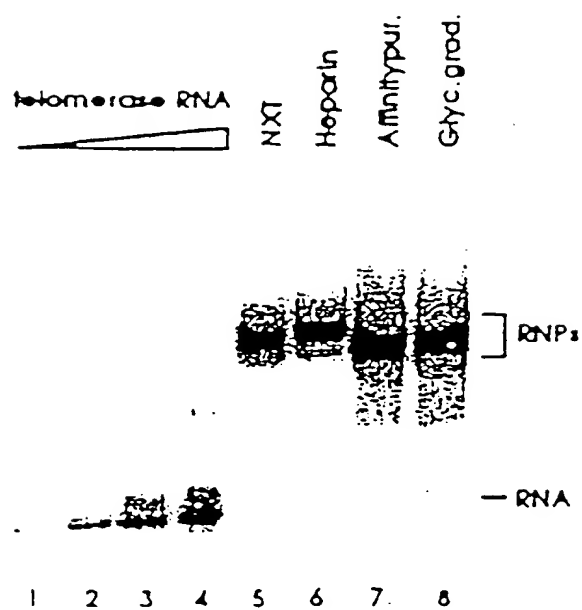
elution with  
displacement oligonucleotide

PANEL B



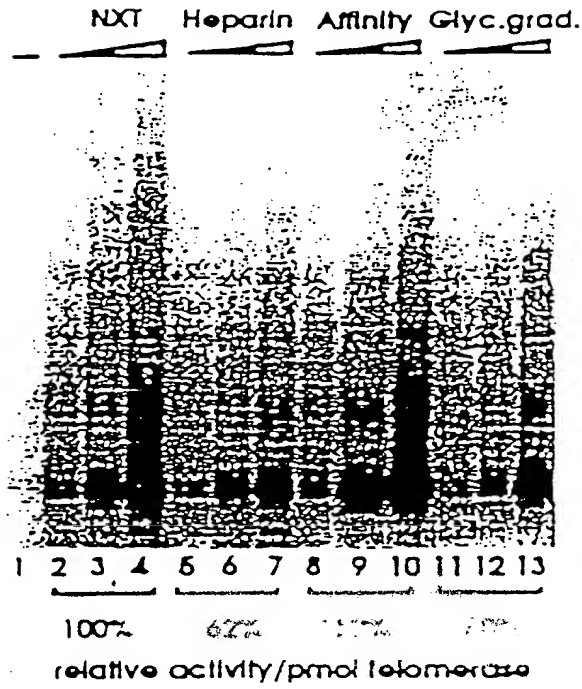
09432503-110299

Figure 27



66207T" ED52E460

Figure 28



66207T" E052E460

Figure 29

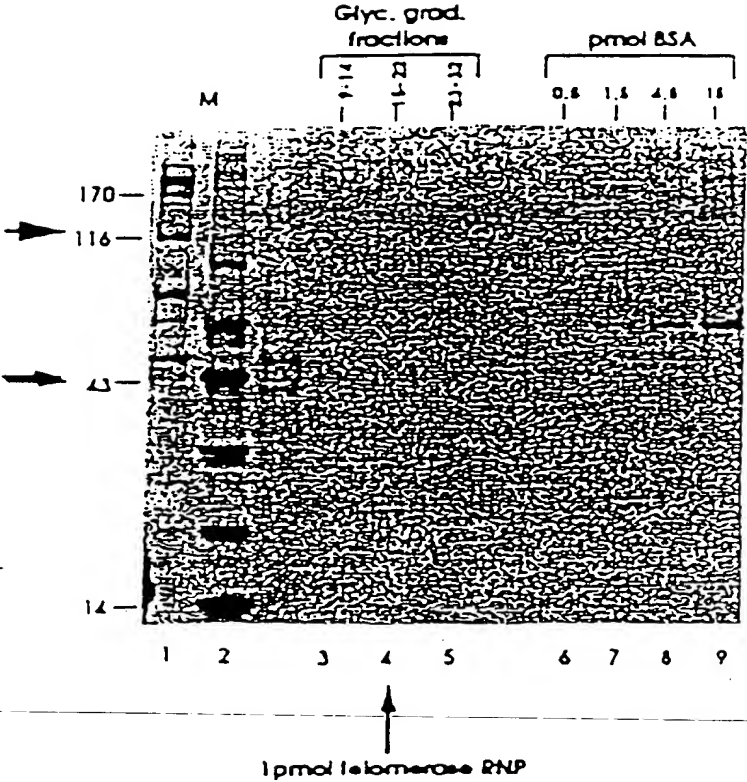


Figure 30

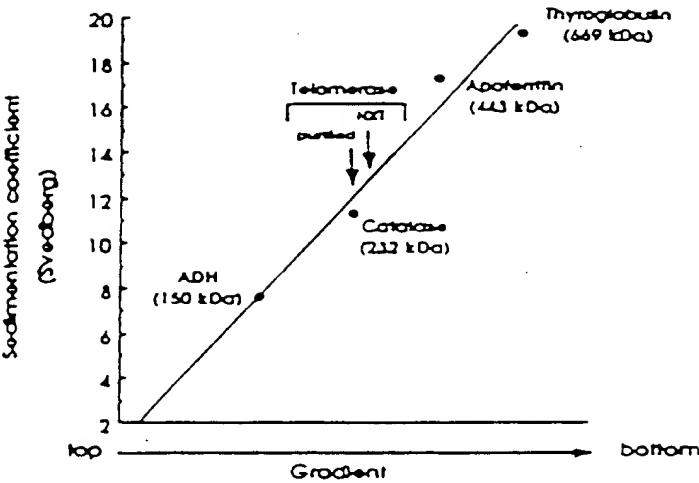


Figure 31 -

00432503 11099

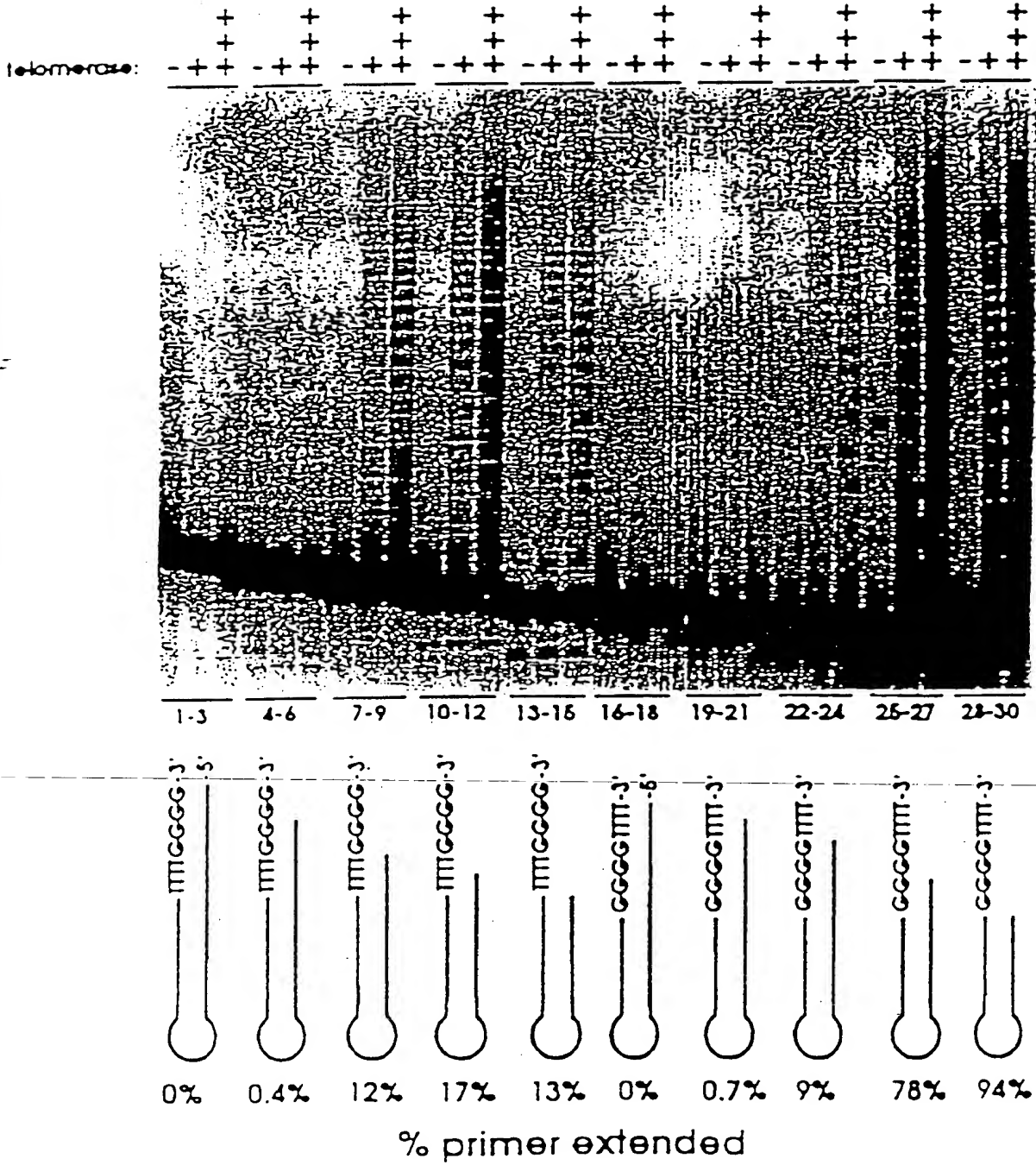


Figure 32

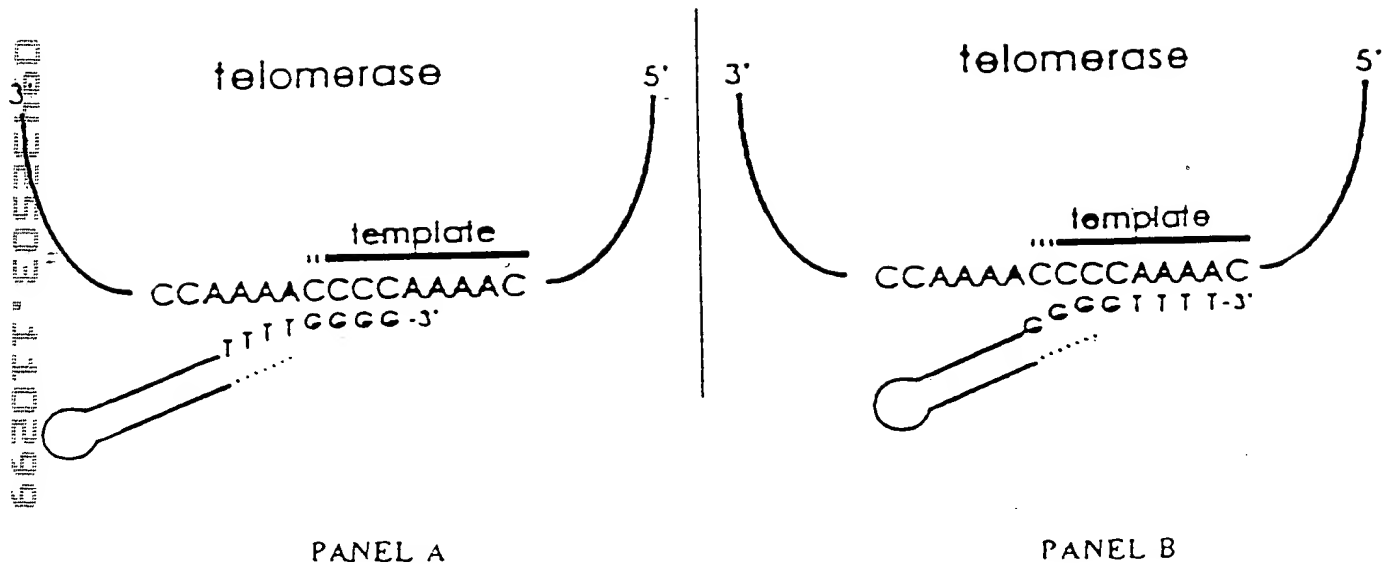
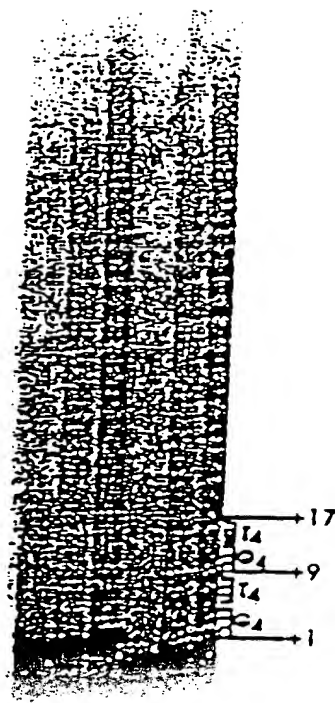


Figure 33



09432503 11029  
66207 E0528460



Figure 34

1 CCCAAAACC CCAAAACCCC AAAACCCCTA TAAAAAAGA AAAAATTGAG  
 51 GTAGTTTAGA AATAAAATAT TATTCCCGCA CAAATGGAGA TGGATATTGA  
 101 TTTGGATGAT ATAGAAAATT TACTTCCTAA TACATTCAAC AAGTATAGCA  
 151 GCTCTTGTAG TGACAAGAAA GGATGCAAAA CATTGAAATC TGGCTCGAAA  
 201 TCGCCTTCAT TGACTATTCC AAAGTTGCAA AAACAATTAG AGTTCTACTT  
 251 CTCGGATGCA AATCTTTATA ACGATTCTTT CTTGAGAAAA TTAGTTTTAA  
 301 AAAGCGGAGA GCAAAGAGTA GAAATTGAAA CATTACTAAT GTTTAAATAA  
 351 AATCAGGTAA TGAGGATTAT TCTATTTTTT AGATCACTTC TTAAGGAGCA  
 401 TTATGGAGAA AATTACTTAA TACTAAAAGG TAAACAGTTT GGATTATTTT  
 451 CCTAGCCAAC AATGATGAGT ATATTAAATT CATATGAGAA TGAGTCAAAG  
 501 GATCTCGATA CATCAGACTT ACCAAAGACA AACTCGCTAT AAAACGCAAG  
 551 AAAAAGTTTG ATAATCGAAC AGCAGAAGAA CTTATTGCAT TTAATTTTCG  
 601 TATGGGTTTT ATTACAATTG TTTTAGGTAT CGACGGTGAA CTCCCGAGTC  
 651 TTGAGACAAT TGAAAAAGCT GTTTACAACG GAAGGAATCG CAGTTCTGAA  
 701 AGTTCTGATG TGTATGCCAT TATTTTGTGA ATTAATCTCA AATATCTTAT  
 751 CTCAATTTAA TGGATAGCTA TAGAAACAAA CCAAATAAAC CATGCAAGTT  
 801 TAATGGAATA TACGTTAAAT CCTTTGGGAC AAATGCACAC TGAATTTATA  
 851 TTGGATTCTT AAAGCATAGA TACACAGAAT GCTTTAGAGA CTGATTTAGC  
 901 TTACAACAGA TTACCTGTTT TGATTACTCT TGCTCATCTC TTATATCTTT  
 951 AAAAGAAGCA GCGGAAATGA AAAGAAGACT AAAGAAAGAG ATTTCAAAAT  
 1001 TTGTTGATTC TTCTGTAACC GGAATTAACA ACAAGAATAT TAGCAACGAA  
 1051 AAAGAAGAAG AGCTATCACA ATCCTGATTC TTAAAGATTT CAAAAATTCC  
 1101 AGGTAAGAGA GATACATTCA TTAATAATTCA TATATTATAG TTTTTCATT  
 1151 CACAGCTGTT ATTTTCTTTT ATCTTAACAA TATTTTTTGA TTAGCTGGAA  
 1201 GTAAAAAGTA TCAAATAAGA GAAGCGCTAG ACTGAGGTAA CTTAGCTTAT  
 1251 TCACATTCAT AGATCGACCT TCATATATCC AATACGATGA TAAGGAAACA  
 1301 GCAGTCATCC GTTTTAAAAA TAGTGCTATG AGGACTAAAT TTTTAGAGTC  
 1351 AAGAAATGGA GCCGAAATCT TAATCAAAAA GAATTGCGTC GATATTGCAA  
 1401 AAGAATCGAA CTCTAAATCT TTCGTTAATA AGTATTACCA ATCTTGATTG  
 1451 ATTGAAGAGA TTGACGAGGC AACTGCACAG AAGATCATT AAGAAATAAA  
 1501 GTAACTTTTA TTAATTAGAG AATAAACTAA ATTACTAATA TAGAGATCAG  
 1551 CGATCTTCAA TTGACGAAAT AAAAGCTGAA CTAAAGTTAG ACAATAAAAA  
 1601 ATACAAACCT TGGTCAAAAT ATTGAGGAAG GAAAAGAAGA CCAGTTAGCA  
 1651 AAAGAAAAAA TAAGGCAATA AATAAAATGA GTACAGAAGT GAAGAAATAA  
 1701 AAGATTTATT TTTTCAATA ATTTATTGAA AAGAGGCGTT TTGGGGTTTT  
 1751 GGGGTTTTGG GG

66207F 0052E460



421 TACTAAAAGGTAAACAGTTTGGATTATTTCCCTAGCCAACAATGATGAGTATATTAAATT  
 ATGATTTTCCATTGTCTCAAACCTAATAAAGGGATCGGTTGTTACTACTCATATAATTAA 480

a Y \* K V N S L D Y F P S Q Q \* \* V Y \* I -  
 b T K R \* T V W I I S L A N N D E Y I K F -  
 c L K G K Q F G L F P \* P T M M S I L N S -

481 CATATGAGAATGAGTCAAAGGATCTCGATACATCAGACTTACCAAAGACAAACTCGCTAT  
 GTATACTCTTACTCAGTTTCTCTAGAGCTATGTAGTCTGAATGGTTTCTGTTTGAGCGATA 540

a H M R M S Q R I S I H Q T Y Q R Q T R Y -  
 b I \* E \* V K G S R Y I R L T K D K L A I -  
 c Y E N E S K D L D T S D L P K T N S L \* -

541 AAAACGCAAGAAAAAGTTTGATAATCGAACAGCAGAAGAAGCTTATTGCATTCTACTATTCG  
 TTTTGCCTTCTTTTCAAACCTATTAGCTTGTCTCTTCTTGAATAACGTAAATGATAAGC 600

a K T Q E K V \* \* S N S R R T Y C I Y Y S -  
 b K R K K K F D N R T A E E L I A F T I R -  
 c N A R K S L I I E Q Q K N L L H L L F V -

601 TATGGGTTTTATTACAATTGTTTTAGGTATCGACGGTGAACCTCCCGAGTCTTGAGACAAT  
 ATACCCAAAATAATGTTAACAAAATCCATAGCTGCCACTTGAGGGCTCAGAACTCTGTTA 660

a Y G F Y Y N C F R Y R R \* T P E S \* D N -  
 b M G F I T I V L G I D G E L P S L E T I -  
 c W V L L Q L F \* V S T V N S R V L R Q L -

661 TGAAAAAGCTGTTTACAACCTGAAGGAATCGCAGTTCTGAAAGTTCTGATGTGTATGCCAT  
 ACTTTTTTCGACAAATGTTGACTTCCTTAGCGTCAAGACTTTCAAGACTACACATACGGTA 720

a \* K S C L Q L K E S Q F \* K F C C V C H -  
 b E K A V Y N \* R N R S S E S S D V Y A I -  
 c K K L F T T E G I A V L K V L M C M P L -

721 TATTTTGTGAATTAATCTCAAATATCTTATCTCAATTTAATGGATAGCTATAGAAACAAA  
 ATAAAACACTTAATTAGAGTTTATAGAATAGAGTTAAATTACCTATCGATATCTTTGTTT 780

a Y F V N \* S Q I S Y L N L M D S Y R N K -  
 b I L \* I N L K Y L I S I \* W I A I E T N -  
 c F C E L I S N I L S Q F N G \* L \* K Q T -

781 CCAAATAAACCATGCAAGTTTAATGGAATATACGTTAAATCCTTTGGGACAAATGCACAC  
 GGTTTATTTGGTACGTTCAAATTACCTTATATGCAATTTAGGAAACCCTGTTTACGTGTG 840

a P N K P C K F N G I Y V K S F G T N A H -  
 b Q I N H A S L M E Y T L N P L G Q M H T -  
 c K \* T M Q V \* W N I R \* I L W D K C T L -

841 TGAATTTATATTGGATTCTTAAAGCATAGATACAGAATGCTTTAGAGACTGATTTAGC  
 ACTTAAATATAACCTAAGAATTTTCGTATCTATGTGTCTTACGAAATCTCTGACTAAATCG 900

a \* I Y I G F L K H R Y T E C F R D \* F S -  
 b E F I L D S \* S I D T Q N A L E T D L A -  
 c N L Y W I L K A \* I H R M L \* R L I \* L -

FIG. 35  
 (CONTINUED)

TTACAACAGATTACCTGTTTTGATTACTCTTGCTCATCTCTTATATCTTTAAAAGAAGCA  
 901 -----+-----+-----+-----+-----+ 960  
 AATGTTGTCTAATGGACAAAATAATGAGAACGAGTAGAGAATATAGAAATTTCTTCGT

a L Q Q I T C F D Y S C S S L I S L K E A -  
 b Y N R L P V L I T L A H L L Y L \* K K Q -  
 c T T D Y L F \* L L L L I S Y I F K R S R -

GGCGAAATGAAAAGAAGACTAAAGAAAGAGATTTCAAATTTGTTGATTCTTCTGTAACC  
 961 -----+-----+-----+-----+-----+ 1020  
 CCGCTTTACTTTTCTTCTGATTTCTTTCTCTAAAGTTTAAACAATAAGAAGACATTGG

a G E M K R R L K K E I S K F V D S S V T -  
 b A K \* K E D \* R K R F Q N L L I L L \* P -  
 c R N E K K T K E R D F K I C \* F F C N R -

GGAATTAACAACAAGAATATTAGCAACGAAAAAGAAGAGCTATCACAATCCTGATTC  
 1021 -----+-----+-----+-----+-----+ 1080  
 CCTTAATTGTTGTTCTTATAATCGTTGCTTTTCTTCTCTCGATAGTGTAGGACTAAG

a G I N N K N I S N E K E E E L S Q S \* F -  
 b E L T T R I L A T K K K K S Y H N P D S -  
 c N \* Q Q E Y \* Q R K R R R A I T I L I L -

TTAAAGATTTCAAAAATTCAGGTAAGAGAGATACATTCATTAAAATTCATATATTATAG  
 1081 -----+-----+-----+-----+-----+ 1140  
 AATTTCTAAAGTTTTTAAGGTCCATTCTCTCTATGTAAGTAATTTAAGTATATAATATC

a L K I S K I P G K R D T F I K I H I L \* -  
 b \* R F Q K F Q V R E I H S L K F I Y Y S -  
 c K D F K N S R \* E R Y I H \* N S Y I I V -

TTTTTCATTTACAGCTGTTATTTTCTTTTATCTTAACAATATTTTGTGATTAGCTGGAA  
 1141 -----+-----+-----+-----+-----+ 1200  
 AAAAAGTAAAGTGTCGACAATAAAAGAAAATAGAATTGTTATAAAAAACTAATCGACCTT

a F F I S Q L L F S F I L T I F F D \* L E -  
 b F S F H S C Y F L L S \* Q Y F L I S W K -  
 c F H F T A V I F F Y L N N I F \* L A G S -

GTAAAAAGTATCAAATAAGAGAAGCGCTAGACTGAGGTAAGTTAGCTTATTCACATTCAT  
 1201 -----+-----+-----+-----+-----+ 1260  
 CATTTTTCATAGTTTATTCTCTTCGCGATCTGACTCCATTGAATCGAATAAGTGTAGTA

a V K S I K \* E K R \* T E V T \* L I H I H -  
 b \* K V S N K R S A R L R \* L S L F T F I -  
 c K K Y Q I R E A L D \* G N L A Y S H S \* -

AGATCGACCTTCATATATCCAATACGATGATAAGGAAACAGCAGTCATCCGTTTTAAAAA  
 1261 -----+-----+-----+-----+-----+ 1320  
 TCTAGCTGGAAGTATATAGGTTATGCTACTATTCCTTTGTCGTCAGTAGGCAAAATTTT

a R S T F I Y P I R \* \* G N S S H P F \* K -  
 b D R P S Y I Q Y D D K E T A V I R F K N -  
 c I D L H I S N T M I R K Q Q S S V L K I -

TAGTGCTATGAGGACTAAATTTTATAGAGTCAAGAAATGGAGCCGAAATCTTAATCAAAAA  
 1321 -----+-----+-----+-----+-----+ 1380  
 ATCAGGATACTCCTGATTTAAAAATCTCAGTTCTTTACCTCGGCTTTAGAATTAGTTTTT

a \* C Y E D \* I F R V K K W S R N L N Q K -  
 b S A M R T K F L E S R N G A E I L I K K -  
 c V L \* G L N F \* S Q E M E P K S \* S K R -

FIG. 35  
 (CONTINUED)



Figure 36

2 EVDYDNOADNHGHSALKTCEEIKEAKTLYSWIQVIRCRNOSOSHYKDL 51  
 19 ELELENOENQNDIQVRVK...IDDPKOY...LVNVTAACLLQEGSYODK 62  
 52 EDIXIFAOTNIVATPRDYNEEDFKVIARKEVF...STGLHIELIDKCLVELL 100  
 63 DERRITKALL...EVAESDPEFICOLAVYIRNELYIRTTTNYIVAF... 107  
 101 SSSDSDROKLOCFCFOLKGNOLAKTHLLTALSTOKOYFFODEWNOVRAM 150  
 108 CVVHKNTOPFIEKYFNKAVLLPNDLLEVCEFAOVLYI 144  
 151 IGNELEFRHLYTKYLI FORTSECTLVQFCGNNVFDHLKVNDKFDKKOKGGA 200  
 145 FDATEFKNLY...LDRILSODIRKELTFRKCLORCVRSKF 181  
 201 ADHNE PRCSTCKYNVKNKEDHFLNNINVPNNNMKSRTTRIFYCTHF 247  
 182 SEFNEYOLGKYCTES...QRKKTMFYLSVTNKOKWDOTKKK... 220  
 248 NRMNOFFKKHEFVSNNKNISAHRAOTIFTNIFRNRIRKKLKDKVIEKI 297  
 221 RKENLLTKLOAIKESDKSKRETG...DIMNVDAIKALKPVMKKI 264  
 298 AYHLEKVKDFNFNYLTCKSCPLPENWRERKOKIENLINKTREEKSKYYEE 347  
 265 AKRONAMK...KHMKAPKIPNSTLESKYLTFKD 294  
 348 LFSYTTDNKCVTOFINEFFYNILPKDFTGRNRKNFQKKVKKYVELNKHE 397  
 295 LIKFEHISEP...KERVYKILGKKYPKTEEEYKAAFQDSASAPFN...PE 338  
 398 LIHKNNLLEKINTREISWMOVETSAXHFYFFDHENIYVLWKLRLWIFEDL 447  
 339 LAGKRNKIEISKWENELSAKGNTAEVWDLNLISSNOLPYHMLRNLN... 386  
 448 VVSLRCFFYVTEQOKSYSKTYYYRKNIWDVIMKHSIADLKKETLAEVQE 497  
 387 ILKAGVSD... 394  
 498 KEVEEWKKS LGFAPGKLRLLPKKTTFRPIMTFNKKIVNSDRKTTKLTNT 547  
 395 TTHS 398  
 548 KLLNSHMLKTLKRNMFKDPFGFAVFNYDDVMKKYEEFVCKWKQVQOPKL 597  
 399 IVINK...ICEPKAVENSKH 415  
 598 FFATNDIEKCYDSVNREKLSTFLKTTKLLSSDFWIMTAQILKRKNIVID 647  
 416 F PLOFFSAIZAVN...EAVTKGFKAKK...RENHNLKQIEAVKE...VVE 457  
 648 SKNFRKKEMKDYFRKFOKIALEGGQYPTLFSVLENEONDLNAKKT LIVE 697  
 458 KTDEKKDM...ELEOTECEGFVKVNEGIGKQYINSIELAIK 496  
 698 AKORNYFKKDNLLQPVINICQYNYINFNGKFKYKQTKGIPQGLCVSSILSS 747  
 497 IAVNKNLDEIKGHTAIFSDVSGSMSTSHSGGAKKYGSVRTCLECALVLGL 546  
 748 FYYATLEESSLGFLRDESMNPENPNVNLLMRLTDDYLLITTOENNAVLFI 797  
 547 MVKORCEKSSFYIFSSPSSQCNKCYLEVDL... 576  
 798 EKLINVSRENGCFKFNHKK...LOTSFPLSPSKFAKYGMDSVEEONIVQDYCD 846  
 577 PGDEL RPSHOKLLOEKGLCGG...TDFPYECIDWTKNKT HVD 617  
 847 WIGISIDHMTLALMPNINLRIEGILCTLNLMQTKKASHWLKXKLSFLM 896  
 618 NIVILSDHMAIEGYS DINVRGSSIVNSI...KKYKDEVN 653  
 897 NNITHYFRKTITTEDFANKTLNKLFI SCGYKYMOCAYEYKD...HFKKNLAM 945  
 654 PNKIF...AVDLECYG...KCLNLGDEFNENNYIKIFGM 687  
 946 SSHIDLEVSKIIYSVTRAFFKYLVCNIKDTIFGEEHYPDFFLSTLKHFI 995  
 688 SDSI...LKFISAKOGGA...NMVE 706  
 996 IFSTKKYIFNRVC 1008  
 707 VI...KNFALOKIG 717

09432500 41099

Figure 37

132 LSTQKOYFFODEWNOVRAHIGNEL FRHLYTKYLIFORTSE . . . . . GTLVQFC 178  
 1 MSRRNO . . . . . KKQAPIGNETNLDVFLQNLVYKSOIEHYKTOQOOI 43  
 179 GNNVFDHLKVNDFDKKOKGGAADHNEPRCCSTCKYNNKNEKDHFLNNIN 228  
 44 KEEDLKLKFKNQDODGNSGNDODDEE . . . . . NNSNKQOELLRRVN 84  
 229 VPNWNNHKSRTIRIFYCTHFNRRNOFFKKHEFVSNKNNISAMDRAQTIFTN 278  
 85 . . . . . OIKQOVOLIKK . . . . . VGSKVEKDLNLDENENKKN 114  
 279 IFRFNRIKKLKDVKIEKIAVHLEKVDNFNYYLTSCPLPENWRERKO 328  
 115 GLSEQQVKEEQLRTITEEQVKYONLVFNMDYQLDLNESGHRHRRRET DY 164  
 329 KIENLINKTREEKSKYYEELFSYTTDNKCVTOFINE . . . . . FFYNILPKDFLTG 377  
 165 DTEKWFEISHDOK . . . . . NYVSIYANQKTSYCWWLKDYFNK 200  
 378 RNRKNFOKKVKYVELNKHLEIHKVLLLEKINTREISWMOVETSAKHFFY 427  
 201 NNYDHLNVSINRLE . . . . . TEAEFYAFDDFSQTIKLTNNSYQTVNID . . . . . 242  
 428 FDHENIYVLWKLRLWI . . . . . FEDLVVSLIRCFYVTEQOKSYSKTYYYRKN 475  
 243 VNFQNNLCILALLRFLLSLERFNILNIRSSY . . . . . TRNQYNFEKIGELLETI 290  
 476 WDVIMKMSIADLKKETLAEOVEKEVEEWKSLGFAFGKLRILPKKTTFRP 525  
 291 FAVVFSHR . . . . . HLOGIHLOVPCEAFQYLVNSSSOISVKDSOLO 330  
 526 IMTFNKXIVNSDRKTTKLTNTKLLNSHMLKTLKNNRMFKDPFGFAVFN 575  
 331 VYSFSTDLKLV . . . . . TNKVQDYFKFLQEFPRLTHVSQAIPVSATNAVENL 378  
 576 DDVKKXEEFVCKWKVQVOPKLF . . . . . FATMDIEKCYDS . . . . . VNREX 615  
 379 NVLLKXVXH . . . . . ANLNLVSIPTQNFQYFVNLOHLKLEFGLEPNILTKOK 426  
 516 LSTFL . . . . . KTKLLSSQFWIMTAQILKRKNNI . . . . . VIDSKNFRKKEHK 657  
 427 LENLLLSIKOSKWLKFLRLNFYTYVAQETSRKOILKOATTIKNLKNNKNO 476  
 558 DYFRONFOXIALECCOYPTLFSVLEN . . . . . EONDNAKKTILIVEAKORNYFX 705  
 477 EETPETKQDSTPSESTSGMKFFDHLSELTELEDFSVN . . . . . LOATOEIY 520  
 706 KDNELQPVNICOYNYINENCKFYKOTKGIPOGLCVSSILSSFFYYATLEE 755  
 521 OSLHKLIRSTNLKKFKESYKYEMEKSKMDTFIDLKNI . . . . . YETLNN 564  
 756 SSLGLRDESNPENPMVNLHRLTDDYLLITTOENNAVLFIKLINVSR 805  
 565 . . . . . LKRCSTNINPHCHISYELTN . . . . . KDSTFYKFKLTINQE 500  
 806 ENGFKFMKKLQTSFPLSPKFAKYCHDSVEEQNIVQDYCDWIGISIDMK 855  
 501 LQHAKYTFK . . . . . ONEFOFMVKSAKIESSSLESLEDIDSLCKSIASCKNLO 648  
 856 TLALMPNINLRIEGILCTLNLMOT . . . . . KKASHWLKK . . . . . KLKSFLMNNITH 901  
 649 NVNI . . . . . ASLLYPNNIQKNPFNKPNNLLFFKQFEOLKNLENVSINC 691  
 902 YFRKTI . . . . . TTEDFANKTLNKLFI SCGYKYMOCAKEYKDHFKKNLAMSSH 948  
 692 ILDOHILNSISEFLEKNNKIKAFILKRYYLLOYLDYTKLFTLOQLPEL 741  
 949 IDLEVSKIISVT . . . . . RAFFKYLVCNIKDT . . . . . IFGEHY 982  
 742 NQVYINOOLEELTVSEVHKQVWENHKQAFYEPLCEFIKESSTLOLIDF 791  
 983 PDFFLS . . . . . TUNHIEIFSTKXY IFNRVCHILKAKEAKLKSDOCOSLIO 1028  
 792 DQNTVSODSIRKILESISESKYNNHYLRNPSOSSSLIKSENEEIQELLK 840

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Figure 38

4 DIDLDIENLLPNTFNKYSSSCSDKKCKTLKSGSKSPSLTIPK..... 47  
617 NVKSAKIESSSLESLEDIDSLCKSIASCKNLQNVNIIASLLYPNNIOKWP 666  
48 LOKOLEFYFSDANLYNDSFLRKLVKSGEORVE..... IETLLH 86  
667 FNKPILLFFKQFEOLKNLENVSINCLDOHILNSISEFLEXNKKIKAFIL 716

65207T" 20923E460



Figure 39

```
1  HEMDIOLDDIENL. . . LPNTFNKYSSSCSDKKGCKTLKSGSKSPS . 42
   | | | | | | | | | | | | | | | | | | | | | | | |
491 IELAIAVKNLDEIKHTAIFSDVSCSHSTSHSGGAKKYGSVRTCLEC 540
   | | | | | | | | | | | | | | | | | | | | | | | |
43  LTIPKLOKO      LEFYFSDANLYNDSFLRKLVLKSGEORVETETLL 85
   | | | | | | | | | | | | | | | | | | | | | | | |
541 ALVLGLMVKORCEKSSFYIFSSPSSOCNKYL.EVDLPGDELRPMSQKLL 589
```

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Figure 41

telomerase p43  
human La  
Xenopus LaA  
Drosophila La  
S. c. Lhlp

LQKQLEFYVSDANLYNDSELRKLVLKSGEQRVEIETLLM  
ICHQVEYVEGDFNLPRDKELKEQI.KLDEGWVPLEIMIK  
ICEQVEYVEGDFNLPRDKELKQOI.LLDDGWVPLETMIK  
ILRQVEYVEGDANLNRDKELREQIGKNEDGWVPLSVLVT  
CLKQVEFYVSEFNFPYDRERRTTAEK.NDGWVPISTIAT

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Figure 42

1 aactcatta attactaatt taatcaacaa gattgataaa aagcagtaaa taaaacccaa  
 61 tagatttaatt tagaaaagta tcaattgaaa aatggaaatt gaaaacaact aagcacaata  
 121 gccaaaagcc gaaaaattgt ggtgggaact tgaattagag atgcaagaaa accaaaatga  
 181 tatataagtt agggtaaga ttgacgatcc taagcaatat ctctggaacg tcactgcagc  
 241 atgtttgtt taggaaggtt gttactacta agataaagat gaaagaagat atatcatcac  
 301 taaagcactt ctgaggttgg ctgagcttga tctgagttc atctgctagt tggcagctta  
 361 catccgtaat gaactttaca tcagaactac cactaactac attgtagcat ttgtgtgt  
 421 ccacaagaat actcaacctt tcatcgaaaa gtacttcaac aaagcagtac ttgtccctaa  
 481 tgacttactg gaagtcctgt aattgcata ggttctctat attttgatg caactgaatt  
 541 caaaaattg tatcttgata ggatacttc ataagatat cgttaaggaa tcactttccg  
 601 taagtgtta caaagatgct tcagaagcaa gttttctgaa tcaacgaat actaacttgg  
 661 taagtattgc actgaatcct aacgtaagaa aacaatgttc cgttacctct cagttaccaa  
 721 caagtaaaag tgggattaaa ctaagaagaa gagaaaagag aatctcttaa ccaaacttta  
 781 ggcaataaag gaatctgaag ataagtcctaa gagagaaact ggagacataa tgaacgttga  
 841 agatgcaatc aaggctttaa aaccagcagt tatgaagaaa atagccaaga gatagaatgc  
 901 catgaagaaa cacatgaagg cacctaaaaa tcttaactct accttggaa caaagtactt  
 961 gaccttcaag gatctatta agttctgcca tattctgag cctaaagaaa gagtctataa  
 1021 gatcttgggt aaaaaatacc ctaagaccga agaggaatac aaagcagcct ttggtgattc  
 1081 tgcacttga ccttcaatc ctgaattggc tggaaagcgt atgaagattg aaatctctaa  
 1141 aacatgggaa aatgaactca gtgcaaaagg caacactgct gaggtttggg ataatttaatt  
 1201 ttaagcaat taactcccat atatggccat gttacgtaac ttgtctaa caactaaagc  
 1261 cgggtttca gatactacac actctattgt gatcaacaag attgtgagc ccaaggccgt  
 1321 tgagaactcc aagatgttcc ctctcaatt ctttagtgcc attgaagctg ttaatgaagc  
 1381 agttactaag ggattcaagg ccaagaagag agaaaataat aatctaaag gtcaaatcga  
 1441 agcagtaaaag gaagttgtt aaaaaaccga tgaagagaag aaagatatgg agttggagta  
 1501 aaccgaagaa ggagaattg taaagtcaa cgaaggaatt ggcaagcaat acattaacct  
 1561 cattgaactt gcaatcaaga tagcagttaa caagaattta gatgaaatca aaggacacac  
 1621 tgcacttctc tctgatgtt ctggttctat gattaccca atgtcaggtg gagccaagaa  
 1681 gtatggctcc gttctactt gtctcgagtg tgcattagtc ctggtttga tggtaaaata  
 1741 acgtttgaa aagttccat tctacatct cagttacct agttctcaat gcaataagtg  
 1801 ttactagaa gttgatctcc ctggagacga actccgtct tctatgtaa aactttgca  
 1861 agagaagga aaacttgggt gtggtactga ttccctat gattgcattg atgaatggac  
 1921 aaagaataaa actcacgtag acaataatgt tattgtct gatatgatga ttgcagaagg  
 1981 atattcagat atcaatgta gaggcagttc cattgttaac agcatcaaaa agtacaagga  
 2041 tgaagtataa cctaacttta aaactttgc agttgactta gaaggttacg gaaagtgcct  
 2101 taatctaggt gatgagttca atgaaaacaa ctacatcaag atattcggta tgagcgattc  
 2161 aatcttaaaag ttacttcag ccaagcaagg aggagcaaat atggtcgaag ttatcaaaaa  
 2221 ctgtccctt caaaaaatag gacaaaagtg agttcttga gattcttca taacaaaaat  
 2281 ctacccctc ttgttttt tattgcatag ccattatgaa atttaaaata ttatctattt  
 2341 attaaagta ctacatagt ttatgtatcg cagtctatta gcctattcaa atgattctgc  
 2401 aaagaacaaa aaagattaaa a

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Figure 43

MEIENNQAQQPKAEKLWWELELEMQENQNDIQVRVKIDDPKQYL  
VNVTAACLLQEGSYQDKDERRYIITKALLEVAESDPEFICQLAVYIRNELYIRTTN  
YIVAFCVVHKNTQPFIEKYFNKAVLLPNDLLEVCEFAQVLYIFDATEFKNLYLDRILS  
QDIRKELTFRKCLQRCVRSKFSEFNEYQLGKYCTESQRKKTMFYLSVTNKQKWDQTK  
KKRKENLLTKLQAIKESEDKSKRETGDIMNVEDAIKALKPAVMKKIAKRQNAMKKHMK  
APKIPNSTLESKYLTFFKDLIKFCHISEPKERVYKJLGKKYPKTEEEYKAAFSDSASAP  
FNPELAGKRMKIEISKTWENELSAKGNTAEVWDNLISNQLPYMAMLRNLSNLIKAGV  
SDTTHSIVTNKICEPKAVENSKMFPLQFFSAIEAVNEAVTKGFKAKKRENMNKLGQIE  
AVKEVVEKTDEEKKDMELEQTEEGEFVKVNEGIGKQYINSIELAIKIAVNKNLDEIKG  
HTAIFSDVSGSMSTMSGGAKKYGSVRTCLECALVLGLMVKQRCEKSSFYIFSSPSSQ  
CNKCYLEVDPGDELRPSMQKLLQEKGKLGGGTDFPYECIDEWTKNKTHTVDNIVILSD  
MMIAEGYSDINVRGSSIVNSIKKYKDEVNPNIKJFAVDLEGYGKCLNLGDEFNENNYI  
KJFGMSDSILKFISAKQGGANMVEVIKNFALQKIGQK

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Figure 44

1 tcaatactat taattaataa ataaaaaaa gcaaaactaca aagaaaatgt caaggcgtaa  
 61 ctaaaaaaag ccataggctc ctataggcaa tgaacaaaat ctgattttg tattacaaaa  
 121 tctagaagtt tacaaaagcc agattgagca ttataagacc tagtagtaat agatcaaaga  
 181 ggaggatctc aagcttttaa agttcaaaaa tttagattag gatggaaact ctggcaacga  
 241 tgaatgatgat gaagaaaaca acitcaataa ataataagaa ttattaagga gagtcaatta  
 301 gattaagtag caagtttaat tgataaaaaa agttgggtct aaggtagaga aagatttgaa  
 361 ttgaacgaa gatgaaaaca aaaagaatgg acmtctgaa tagcaagtga aagaagagta  
 421 attagaacg attactgaag aataggttaa gtattaaaa ttagtattt acatggacta  
 481 ccagttagat tttaatgaga gtgggggcca tagaagacac agaagagaaa cagattatga  
 541 tactgaaaaa tggtttgaaa tatctcatga ccaaaaaaat tatgtatcaa ttacgccaa  
 601 ctaaaagaca tcatatgtt gggtggctaa agattatmt aataaaaaa attatgatca  
 661 tcttaatgta agcatlaaca gactagaaac tgaagccgaa ttctatgcct ttgatgatt  
 721 ttcaaaaaca atcaaaacta ctaataatc ttactagact gttacatag acgttaatt  
 781 tgataataat ctctgtatc tcgcatngct tagattmta ttactactag aaagattcaa  
 841 tatttgaaat ataagatctt ctatataag aaattaalat aatttgaga aaattgggtga  
 901 gctactgaa actatctcg cagttgtctt ttctatcgc cactacaag gcattcatt  
 961 acaagttct tgcgaagcgt tctaatatt agttaactc tcatcataa ttgctgtaa  
 1021 agatagctaa ttataggat acitmtctc tacagactta aaattagttg acactaaca  
 1081 agtccaagat tatttaagt tctataaga attccctcgt ttgactcatg taagctagta  
 1141 ggctatccca gttagtgtc ctacgcgtg agagaacctc aatgtttac ttaaaaaggt  
 1201 caagcatgct aatctaat tagttctat cctaccta ttcaatttg atttctact  
 1261 tgttaatta taacattga aattagagt tggattagaa ccaaatatt tgacaaaaca  
 1321 aaagctgaa aatctactt tgagtataa ataataaaa aatcttaaat tttaagatt  
 1381 aaactttac acctacgtt ctaagaac ctccagaaaa cagatattaa aacaagctac  
 1441 aacaatcaa aatctcaaaa acaataaaaa tcaagaagaa actcctgaaa cttaagatga  
 1501 aactccaagc gaaagcaca gtggtatgaa attttgat catctmtc aattaaccga  
 1561 gctgaagat ttacgctta actgtgaag taccgaagaa atttatgata gcttgcacaa  
 1621 actttgat agatcaaca attaaagaa gttcaaatla agttacaaat atgaaatgga  
 1681 aaagagttaa atggatacat tcatagatct taagaatatt tatgaaacct taaacaatct  
 1741 taaagatgc tctgttaata tatcaaatc tcatggaaac attcttatg aactgacaaa  
 1801 taaagattct actttata aattaaagt gaccttaaac taagaattat aacacgctaa  
 1861 gtatacttt aagtagaacg aatttaatt taataacgtt aaaagtgc aaattgaatc  
 1921 ttccatla gaaagcttag aagatattga tagtcttgc aaatctattg cttctgtaa  
 1981 aaattacaa aatgttaata ttatcgccag ttgtcttat cccaacaata tttagaaaa  
 2041 tctmcaat aagcccaatc ttctattt caagcaatt gaataattga aaaattgga  
 2101 aaatgtatct atcaactgta ttctgatca gcatatactt aattctatt cagaattct  
 2161 agaaaaaat aaaaaataa aagcatlcat ttgaaaaga tattattat tacaattat  
 2221 tctgattat actaaattat taaaacact tcaatagtt cctgaattaa attagttta  
 2281 catlaantag caattagaag aattgactgt gagtgaagta cataagtaag tatgggaaaa  
 2341 ccacaagcaa aaagctttct atgaaccatt atgtgagtt atcaagaat catcctaaac  
 2401 ccttagcta atagatttg accaaaacac tgaagtgtat gactctatta aaaagattt  
 2461 agaattctata tctgagtcta agtatcatca ttattgaga ttgaacctta gttatctag  
 2521 cagtttaatt aaatctgaaa acgaagaaat ttaagaactt ctcaaagctt gcgacgaaaa  
 2581 aggtgttta gtaaaagcat actataaatt cccctatgt ttaccaactg gtacttatta  
 2641 cgattacaat tcatagatag ggtgattaat taaatattag ttaataaaa tattaaatat  
 2701 tgaatattc ttgcttatt attgaataa tacaataaat agtcaattt agtgtttga  
 2761 atataattt gttattaat tcatattt aagtaataa ttatttca atcatmtt  
 2821 aaaaaatcg

Figure 45

MSRRNQKKPQAPIGNETNLDFVLQNLEVYKSQIEHYKTQQQIK  
EEDLKLLKFKNQDQDGNNGNDDDEENNSNKQQELLRRVNQIKQQVQLIKKVGSKVEK  
DLNLNEDENKKNGLSEQQVKEEQLRTITEEQVKYQNLVFNMDYQLDLNESGGHRRHRR  
ETDYDTEKWFEISHDQKNYVSIYANQKTSYCWWLKDYFNKNNYDHLNVNINRLETEAE  
FYAFDDFSQTIKLTNNSYQTVNIDVNFNNLCILALLRFLLSLERFNLNIRSSYTRN  
QYNFEKIGELLETFVVFVSHRHLQGIHLQVPCEAFQYLVNSSSQISVKDSQLQVYSF  
STDCLKLVDTNKVQDYFKFLQEFPRLTHVSQQAIPVSATNAVENLNVLLKKVKHANLNL  
VSIPTQFNDFYFVNLQHLKLEFGLLEPNILTKQKLENLLLSIKQSKNLKFLRLNFYTY  
VAQETSRKQILKQATTIKNLKNNKNQEETPETKDETPSESTSGMKFFDHLSELTELED  
FSVNLQATQEIYDSLHKLLIRSTNLKKFKLSYKYEMEKSKMDTFIDLKNIYETLNNLK  
RCSVNISNPHGNISYELTNKDSTFYKFKLTLNQELQHAKYTFKQNEFQFNNVKSADIE  
SSSLESLEDIDSLCKSIASCKNLQNVNIIASLYPNNQSTISNKKPDLFFKQFEQLK  
NLENVSINCILDQHILNSISEFLEKNKKIKAFILKRYLLQYYLDYTKLTKLQQLPE  
LNQVYINQQLLEELTVSEVHKQVWENHKQKAFYEPLCEFIKESQTLQLIDFDQNTVSD  
DSIKKILESISESKYHHYLRNPSQSSSLIKSENEEIQELLKACDEKGVLVKAYYKFP  
LCLPTGTYYDYNSDRW

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Figure 46

MKILFEFIQDKLDIDLQTNSTYKENLKCGHFNGLDEILTTCFAL  
PNSRKIALPCLPGDLSHKAVIDHCIIYLLTGELYNNVLTFGYKIARNEDVNNSLFCBS  
ANVNVTLKGAAWKMFHSLVGTYAFVDLLINYTVIQFNGQFFTQIVGNRCNEPHLPPK  
WVQRSSSSSATAAQIKQLTEPVTNKQFLHKLNNSSFFPYSKILPSSSSIKKLTDLR  
EAIFPTNLVKIPQRLKVRNLTQKLLKRHKRLNYVSILNSICPPLEGTVLDLSHLR  
QSPKERVLFKFIIVILQKLLPQEMFGSKKNKGKJIKNLNLLSLPLNGYLPFDSLLKKL  
RLKDFRWLFISDIWFTKHNFENLNQLAICFISWLFRLIPKJIQTFFYCTEISSTVTI  
VYFRHDTWNKLITPFIVEYFKTYLVENNVCRNHNSYTLNHNHSMRJIIPKKSNNFR  
IIAIPCRGADEEEFTIYKENHKNAIQPTQKILEYLRNKRPTSFTKJYSPTQIADRIKE  
FKQRLKKFNVLPELYFMKFDVKSCYDSIPRMECMRILKDALKNENGFFVRSQYFFN  
TNTGVLKLFNVNASRVPKPYELYIDNVRTVHLSNQDVINVVEMEIFTALWVEDKCY  
IREDGLFQGSSLSAPIVDLVYDDLLEFYSEFKASPSQDTLILKLADDFLIISTDQQQV  
INIKKLAMGGFQKYNAKANRDKJLAVSSQSDDDTVIQFCAMHIFVKELEVWKHSSTMN  
NFHIRSKSSKGIFRSLIALFNTRISYKTIDTNLNSTNTVLMQIDHVVKNISECYKSAF  
KDLSINVTQNMQFHSFLQRIIEMTVSGCPITKCDPLIEYEVRFITLNGFLESLSNTS  
KFKDNIILLRKEIQHLQAYIYIYIHVN

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"E02E460"



Figure 47

*Oxytricha*  
*Euplotes*

LCVSYILSSFYYANLEENALQFLRKESMDPEKPETNLLMRLT  
LCVSSILSSFYYATLEESSLGFLRDESMNPENPNVNLLMRLT

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Figure 48

ATTTATACTCATGAAAATCTTATTTCGAGTTCATTCAAGACAAGCTTGACATTGATCTACA  
 GACCAACAGTACTTACAAAGAAAATTTAAAATGTGGTCACTTCAATGGCCTCGATGAAAT  
 TCTAACTACGTGTTTCGCACTACCAAATTCAGAAAAATAGCATTACCATGCCTTCCTGG  
 TGACTTAAGCCACAAAGCAGTCATTGATCACTGCATCATTTACCTGTTGACGGGCGAATT  
 ATACAACAACGTACTAACATTTGGCTATAAAAATAGCTAGAAATGAAGATGTCAACAATAG  
 TCTTTTTTGGCATTCTGCAAATGTAAACGTTACGTTACTGAAAGGCGCTGCTTGAAAAAT  
 GTTCCACAGTTTGGTCGGTACATACGCATTTCGTTGATTTATTGATCAATTATACAGTAAT  
 TCAATTTAATGGGCAGTTTTTCACTCAAATCGTGGGTAACAGATGTAACGAACCTCATCT  
 GCCGCCCCAAATGGGTCCAACGATCATCCTCATCATCCGCAACTGCTGCGCAAATCAAACA  
 ACTTACAGAACCAGTGACAAATAAACAATTCTTACACAAGCTCAATATAAATTCCTCTTC  
 TTTTTTTCCTTATAGCAAGATCCTTCCTTCATCATCATCTATCAAAAAGCTAACTGACTT  
 GAGAGAAGCTATTTTTCCCACAAATTTGGTTAAAATTCCTCAGAGACTAAAGGTACGAAT  
 TAATTTGACGCTGCAAAAGCTATTAAGAGACATAAGCGTTTGAATTACGTTTCTATTTT  
 GAATAGTATTTGCCACCATTGGAAGGGACCGTATTGGACTTGTGCGATTGTGAGTAGGCA  
 ATCACCAAAGGAACGAGTCTTGAAATTTATCATTTGTTATTTTACAGAAGTTATTACCCCA  
 AGAAATGTTTGGCTCAAAGAAAAATAAGGAAAAATTTATCAAGAATCTAAATCTTTTTATT  
 AAGTTTACCCTTAAATGGCTATTTACCATTGTGATAGTTTGTGAAAAAGTTAAGATTAAA  
 GGATTTTCGGTGGTTGTTTCTGATATTTGGTTACCAAGCACAATTTTGAAAACCTT  
 GAATCAATTGGCGATTTGTTTCTTTCTGGCTATTTAGACAATAATCCCAAAATTAT  
 ACAGACTTTTTTTTACTGCACCGAAATATCTTCTACAGTGACAATTGTTTACTTTAGACA  
 TGATACTTGAATAAACTTATCACCCCTTTTATCGTAGAATATTTTAAGACGTACTTAGT  
 CGAAAACAACGTATGTAGAAACCATAATAGTTACACGTTGTCCAATTTCAATCATAGCAA  
 AATGAGGATTATACCAAAAAAAGTAATAATGAGTTCAGGATTATTGCCATCCCATGCAG  
 AGGGGCAGACGAAGAAGAAATTCACAATTTATAAGGAGAATCACAAAAATGCTATCCAGCC  
 CACTCAAAAAATTTTAGAATACCTAAGAAACAAAAGGCCGACTAGTTTTACTAAAATATA  
 TTCTCCAACGCAAATAGCTGACCGTATCAAAGAATTTAAGCAGAGACTTTTAAAGAAATT  
 TAATAATGTCTTACCAGAGCTTTATTTTATGAAATTTGATGTCAAATCTTGCTATGATTC  
 CATACCAAGGATGGAATGTATGAGGATACTCAAGGATGCGCTAAAAAATGAAAATGGGTT  
 TTTTCGTTAGATCTCAATATTTCTTCAATACCAATACAGGTGTATTGAAGTTATTTAATGT  
 TGTTAACGCTAGCAGAGTACCAAAACCTTATGAGCTATACATAGATAATGTGAGGACGGT  
 TCATTTATCAAATCAGGATGTTATAAACGTTGTAGAGATGGAAATATTTAAAAACAGCTTT  
 GTGGGTTGAAGATAAGTGCTACATTAGAGAAGATGGTCTTTTTTCAGGGCTCTAGTTTATC  
 TGCTCCGATCGTTGATTGTTGATGACGATCTTCTGGAGTTTTATAGCGAGTTTAAAGC  
 CAGTCCTAGCCAGGACACATTAATTTTAAACTGGCTGACGATTTCTTATAATATCAAC  
 AGACCAACAGCAAGTGATCAATATCAAAAAGCTTGCCATGGGCGGATTTCAAAAATATAA  
 TGCGAAAGCCAATAGAGACAAAATTTTAGCCGTAAGCTCCCAATCAGATGATGATACGGT  
 TATTCAATTTTGTGCAATGCACATATTTGTAAAGAATTGGAAGTTTGGAACATTCAAG  
 CACAATGAATAATTTCCATATCCGTTTCGAAATCTAGTAAAGGGATATTTCGAAGTTTAAAT  
 AGCGCTGTTTAACTAGAAATCTCTTATAAAACAATTGAGACAAATTTAAATTCAACAAA  
 CACCGTTCTCATGCAAATTGATCATGTTGTAAAGAACATTTTCGGAATGTTATAAATCTGC  
 TTTTAAGGATCTATCAATTAATGTTACGCAAAATATGCAATTTTATTTCGTTCTTACAACG  
 CATCATTGAAATGACAGTCAGCGGTTGTCCAATTACGAAATGTGATCCTTTAATCGAGTA  
 TGAGGTACGATTACCATATTGAATGGATTTTGGAAAGCCTATCTTCAAACACATCAA  
 ATTTAAAGATAATATCATTCTTTTGAGAAAGGAAATTCAACACTTGCAAGC

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Figure 49

AKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKS VWSKLQSIGIRQHLKR  
VQLRDVSEAEVRQHQREARPA LLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKR  
AERLTSRVKALFSVLNYERA

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SECRET

Figure 50

GCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTC  
TTTCTTTTATGTCACGGAGACCACGTTTCAAAGAAGACAGGCTCTTTTTCTACC  
GGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAA  
GAGGGTGCAGCTGCGGGACGTGTCGGAAGCAGAGGTCAGGCAGCATCGGGA  
AGCCAGGCCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGACG  
GGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCG  
CAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGC  
GTGCTCAACTACGAGCGGGCGCG

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Figure 51

MTEHHTPKSRJLRFLNQYVYLCTLNDYVQLVLRGSPASSYSNICERLRSDVQTSFSIFLHSTVVGF  
DSKPDEGVQFSSPKCSQSELIANVVKQMFDESFERRRNLLMKGFSMNHEDFRAMHVNGVQNDLV  
STFPNYLISILESKNWQLLLEIIGSDAMHYLLSKGSIFEALPNDNYLQISGIPLFKNNVFEETVSKKRK  
RTIETSITQNK SARKEVSWNSISISRFSIFYRSSYKKFKQDLYFNLHSICDRNTVHMWLQWIFPRQFG  
LNAFQVKQLHKVIPLVSQSTVVPKRLLKVYPLIEQTAKRLHRISLSKVYNHYCPYIDTHDDEKILS  
YSLKPNQVFAFLRSILVRVFPKLIWGNQRIFEIILKDLETFLKLSRYESFSLHYLMSNIKISEIEWLVL  
GKRSNAKMCLSDFEKRKQIFAEFIYWL YNSFIIPILQSFFYITESSDLRNRTVYFRKDIWKLLCRPFIT  
SMKMEAFEKINENNVRMDTQKTTLP PAVIRLLPKKNTFRLITNLRKRFLIKMGSNKKMLVSTNQT  
LRPVASILKHLNEESSGIPFNLEVYMKLLTFKKDLLKHRMFGRKKYFVRIDIKSCYDRIKQDLMFR  
IVKKKLLKDPEFVIRKYATIHATSDRATKNFVSEAFSYFDMVPFEKV VQLLSMKTSDTL FVDVFDY  
WTKSSSEIFKMLKEHLSGHIVKIGNSQYLQKVGIPQGSILSSFLCHFYMEDLIDEYLSFTKKKGSVL  
LRVVD DFLFITVNKKDAKKFLNLSLRGFEEKNFSTSL EKTVINFENSNGIINNTFFNESKKRMPFFG  
FSVNMRLD TLLACPKIDEALFNSTSVELTKHMGKSFFYKILRSSLASFAQVFIDITHNSKFNSCCNI  
YRLGYSMCMRAQAYLKRMDIFIPQRMFITDLLNVIGRKIWKKLA EILGYTSRRFLSSAEVKWLFC  
LGMRDGLKPSFKYHPCFEQLIYQFQSLTDLIKPLRPVLRQVFLHRRJAD

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Figure 52

ggtaaccgaattacmccmccataagcctaattgcttccctgaacgcctcctaaatctctggaaatattttacaagaacicaataacaataccaagicaaattccaatatgaagg  
 tgnattagigatcgataatatttatttaccggtacccaagataaggacaaaagaacaaacttccccctaaagacmmtatttatttatttcaaatatatttcg  
 ggncgcttatttatttctggtactgttttagctgctacttctagccaaccgctgttctaccccgicantggatatagctcnggagtagctcacagaaatccttacaatctt  
 ctgatgagactatattagattacattacagtcggtgcatatttcaaacatggagcccttaccatttagatgagtcacgtcgcatgatggagtagtggatcatccaacgttgcctng  
 aaaagnggataattttgcaaaatcatgiccttagtgggtggaatccgcgaaggttttgatgctngcacacgtctagcatgattgagatattcaaaaatttattccactacaa  
 ctccttaacgcggmtatttctatttctatttctatgntgntccaaatattgattcatctcgtattaggcttttccggtttacttctggaatcgtaacmmtcactattccccctaatg  
 aataatcctaattagmccgcttataatgtagtagtagaagattgggtattctactcgttgaatgntattagmtaagatactmgcaaaacatttagtctatcattatataaaa  
 aaaatcctataattataataataatcaatattgggtcactatttataaaacgntatgatcagtaggacacmgtcalatatatagttatgntaalggttactngtaacngcA T  
 GACCGAACACCATACCCCCAAAAGCAGGATTCTTCGCTTTCTAGAGAATCAATATGTATACCTATGTAT  
 CCTTAAATGATTATGTACAACCTTGTCTTGTGAGAGGGTCGCCGGCAAGCTCGTATAGCAATATATGCGAA  
 CGCTTGAGAAGCGATGTACAACCGTCTTTTCTATTTTCTTCACTCGACTGTAGTCGGCTTCGACAGT  
 AAGCCAGATGAAGGTGTTCAATTTTCTTCTCCAAAATGCTCACAGTCAAGAGgtatatattttggttgggttttctatctg  
 ggtagctaatatatgggcagCTAATAGCGAATGTTGTAAAACAGATGTTTCGATGAAAGTTTTGAGCGTCGAAGGA  
 ATCTACTGATGAAAGGGTTTTCCATGgttaaggtaattgtgaaatattaccgtcaattactgttcaaagagangtatttaaccgataaagAA  
 TCATGAAGATTTTCGAGCCATGCATGTAAACGGAGTACAAAATGATCTCGTTTCTACTTTTCTTAATTA  
 CCTTATATCTATACTTGAGTCAAAAAATTGGCAACTTTTGTAGAAAATgttaataaccggtaagaatgntgctgcacmmtgaaca  
 agactgacaagtagTATCGGCAGTGTATGCCATGCATTACTTATTAATCCAAAGGAAGTATTTTGTAGGCTCTTC  
 CAAATGACAATTACCTTCAGATTTCTGGCATACCACTTTTAAAAATAATGTGTTTGAGGAAACTGTGT  
 CAAAAAAGAAAGCGAACCATTGAAACATCCATTACTCAAAATAAAAGCGCCCCGCAAGAAGTTTC  
 CTGGAATAGCATTCAATTAGTAGGTTTAGCATTTTTTACAGGTCATCCTATAAGAAGTTTAAGCAAGgt  
 aactaatactgntatcctcctataactaattmagATCTATATTTTAACTTACACTCTATTTGTGATCGGAACACAGTACACATG  
 TGGCTTCAATTGGATTTTTTCCAAGGCAATTTGGACTTATAAACGCATTTCAAGTGAAGCAATTTGCACAA  
 AGTGAATTCCTGGTATCACAGAGTACAGTTGTGCTCCCAACGCTCCTTAAGGTATACCTTTTAATTGA  
 ACGAACAGCAAAAGCGACTCCATCGTATTTCTCTATCAAAAGTTTACAACCATTATTGCCCATATATTGA  
 CACCCACGATGATGAAAAAATCCTTAGTTATTCCTTAAAGCCGAACCAGGTGTTTGCCTTTCTTCGATC  
 CATTCTTGTTCGAGTGTTCCTAAATTAATCTGGGGTAACCAAAGGATATTTGAGATAATATTAAGGg  
 tattgtataaaattattaccactaacgatttaccagACCTCGAAACTTTCTTGAAATTATCGAGATACGAGTCTTTTAGTTTAC  
 ATTATTTAATGAGTAACATAAAAGgtaatatgccaaatttttaccantaatttaacaatcagATTTTCAGAAATTGAATGGCTAGT  
 CTTTGGAATAAGGTCAAAATGCGAAAAATGTGCTTAAGTGAATTTGAGAAACGCAAGCAAAATATTTGCGG  
 AATTCATCTACTGGCTATACAATTCGTTTATAATACCTATTTTACAATCTTTTTTTTATATCACTGAATC  
 AAGTGATTTACGAAATCGAACTGTTTATTTTAGAAAAGATATTTGAAACTCTTGTGCCGACCCTTTAT  
 TACATCAATGAAAAATGGAAGCGTTTGAAAAAATAAACGAGgtattttaaagatttttgcaaaagcctaatttcagAACAA  
 TGTTAGGATGGATACTCAGAAAACCTACTTTGCCTCCAGCAGTTATTCGTCTATTACCTAAGAAGAATAC  
 CTTTCGTCTCATTACGAATTTAAGAAAAAGATTCTTAATAAAAGgtataattttggtatcaatgtaacmmtcacttattatag  
 cagATGGGTTCAACAAAAAAATGTTAGTCAGTACGAACCAAACTTTACGACCTGTGGCATCGATACTG  
 AAACATTTAATCAATGAAGAAAGTAGTGGTATTCATTTAACTTTGGAGGTTTACATGAAGCTTCTTACT  
 TTTAAGAAGGATCTTCTTAAGCACCGAATGTTTGgttaattataatgctgcgctcctattataatttcagGCGTAAGAAG  
 TATTTTGTACGGATAGATATAAAATCCTGTTATGATCGAATAAAGCAAGATTTGATGTTTCGGATTGTT  
 AAAAAAGAACTCAAGGATCCCGAATTTGTAAATTCGAAAGTATGCAACCATACATGCAACAAGTGACCG  
 AGCTACAAAAAACTTTGTTAGTGAGGCGTTTTCTATTgttaagmttttctcnggaatttttaacaatccttttagTTGATAT  
 GGTGCCTTTTGAAAAAGTCGTGCAGTTACTTTCTATGAAAACATCAGATACTTTGTTTGTGATTTTGT  
 GGATTATTGGACCAAAAGTTCTTCTGAAATTTTTAAATGCTCAAGGAACATCTCTCTGGACACATTGT  
 TAAAGgtataccaattgngaattgtaataacactaatgaaactagATAGGAAATTCTCAATACCTTCAAAAAGTTGGTATCCCTC  
 AGGGCTCAATTCTGTCTATCTTTTTTGTGTCTATATATGGAAGATTTGATTGATGAATACCTATCGTT  
 TACGAAAAAGAAAGGATCAGTGTGTTACGAGTAGTCGACGATTTCTCTTTTATAACAGTTAATAAAA  
 AGGATGCAAAAAAATTTTTGAATTTATCTTTAAGAGgttagtgcgtcctcctaaagtttaaccgttgaagGATTTGAGAA  
 ACACAATTTTTCTACGAGCCTGGAGAAAAACAGTAATAAACTTTGAAAAATAGTAATGGGATAATAACA  
 ATACTTTTTTTAATGAAAGCAAGAAAAAGAAATGCCATTCTTCGGTTTTCTCTGTGAACATGAGGTCTCTTG  
 ATACATTGTTAGCATGTCCTAAAAATGATGAAGCCTTATTTAACTCTACATCTGTAGAGCTGACGAAAC  
 ATATGGGGAAATCTTTTTTTTACAAAAATCTAAAGgtatactgtgaacgaataatgctgacaaataatcagATCGAGCCTTGC  
 ATCCTTTGCACAAGTATTTATTGACATTACCCACAATTCAAAATTCATTCTTGCTGCAATATATATAG  
 GCTAGGATACTCTATGTGTATGAGAGCACAAGCATACTTAAAAAGGATGAAGGATATATTTATCCCC  
 AAAGAATGTTTCATAACGGgtgagtactattttaaactagaaaagcctaatttaacattagATCTTTTGAATGTTATTGGAAGAAAA  
 ATTTGGAATAAGTTGGCCGAAATATTAGGATATACGAGTAGGCGTTTCTTGTCTCTGCAGAAGTCAA

0943503.10299

Figure 52 (cont.)

ATGgtacgtgicggctcagagacacagcaatatgacacacagGCTTTTTGTCTTGGGAATGAGAGATGGTTTGAAACCCTCTT  
TCAAATATCATCCATGCTTCGAACAGCTAATATACCAATTTTCAGTCATTGACTGATCTTATCAAGCCGC  
TAAGACCAGTTTTGCGACAGGTGTTATTTTTACATAGAAGAAATAGCTGATTAAAtgicamcaamantataacacitct  
tattaciggtgicntaaacaatatattactaagiatagctgacccccaaagcaagcatactataggamcttagtaaagtaaaantaatcicgnanagmngangacngtctn  
atccntatactntaagaaagangacagiggtgctgactacigcccacatgccantaaacgggagtggttaaacantaaaagtaatacatgaggctaatciccmcamtag  
aataaggaaagtggtmctataatgaataatgcccgcactaatgcaaaaagacgaagantatcncntaaacaaggggantaaagcataiccgaaaggaaaagagagtaata  
accagtggtggaagaaagcaaggataamtggaacaagcncigcagatgacaggctaaamtggtgaccgaamtggtaaaagccccaggntatccatgggtggccg  
gcnngctactgagacgaaaagaaactaaggatagmgaatactaatagctcattaatgicntataaagmngmncctgacticaamngcatgggtgaaaagaaata  
gtgtaagccantngganccgaaatagccaaantcnggncctcaaaagcggaggtctaaagaactatngaagcmtatgaggcncaaaaactcctcctgattaaaggag  
gaatctccaccgatgaggaaatggatagcmtatcagctgctgaggagaagcctaamttmgcaaaaagaaaatcatgggagacatcctngatgaatcagatcgga  
gagtatccagcggatccngatgicataactcattmctgaaatgtatggctcactgctcgttcgactcctgactcctacgcagtaagtgaccaaggtacc

09432503.110299

Figure 53

EST2 pep	FFYCTEISST	VTIVYFRHDT	WN----	KLIT	P-----	FIVE	YFK-TYLVEN	40
Euplotes pep	FFYVTEQOKS	YSKTYYYRKN	IWDVI-MKMS	IAD----	LKK	ETLA--EVOE		43
Trans of tetrahymen	-----KHKE	GSQIFYRKP	IWKLVSKLTI	VKVRIQFSEK	NKQMGNFYQ			44
Consensus	FFY.TE..K.	.S..YYRK.	IW....KL..	.....F..K	.....V..			50
EST2 pep	NVCRNHNSY-	-----	TLSNFNHSN	RIIPKSNNE	RIIPKSNNE	RIIPKSNNE		79
Euplotes pep	KEVEEWKKS	-----	GFAPGGL	RIIPKSNNE	RIIPKSNNE	RIIPKSNNE		78
Trans of tetrahymen	KIQLEENLE	KVEEKLIPE	SFOKYPQGL	RIIPKSNNE	RIIPKSNNE	RIIPKSNNE		92
Consensus	K...E.....	-----	....F..G	RIIPKSNNE	RIIPKSNNE	RIIPKSNNE		100
EST2 pep	ADEEFTIYK	ENHQNAIQPT	QKILEYRNK	RPTSFTKIYS	PTQIADRIKE			129
Euplotes pep	IVNSDRKTTK	LTNTKLLNS	HLMLKTLKN	-----RMFK	-DPFGFAVFN			120
Trans of tetrahymen	DKQKNIK---	LNLNQILMDS	QLVFRNLKD	-----ML-G	-QXIGYSVFD			130
Consensus	.....K..K	LN.N..L..S	QL.L..LKN	-----	..IG..VF.			150
EST2 pep	FKQRLLEKN	NVL-----	EFVCKWKQVG	QKIEFFATMD	TEKCYD			157
Euplotes pep	YD-DVMDKVE	EFVCKWKQVG	QKIEFFATMD	TEKCYD				155
Trans of tetrahymen	NK-QISEKFA	QFIEKWKQVG	QKIEFFATMD	TEKCYD				158
Consensus	.K-...KKE	.F..KWK..G	E..L..T..D	...CYD				186

662017-0052E460



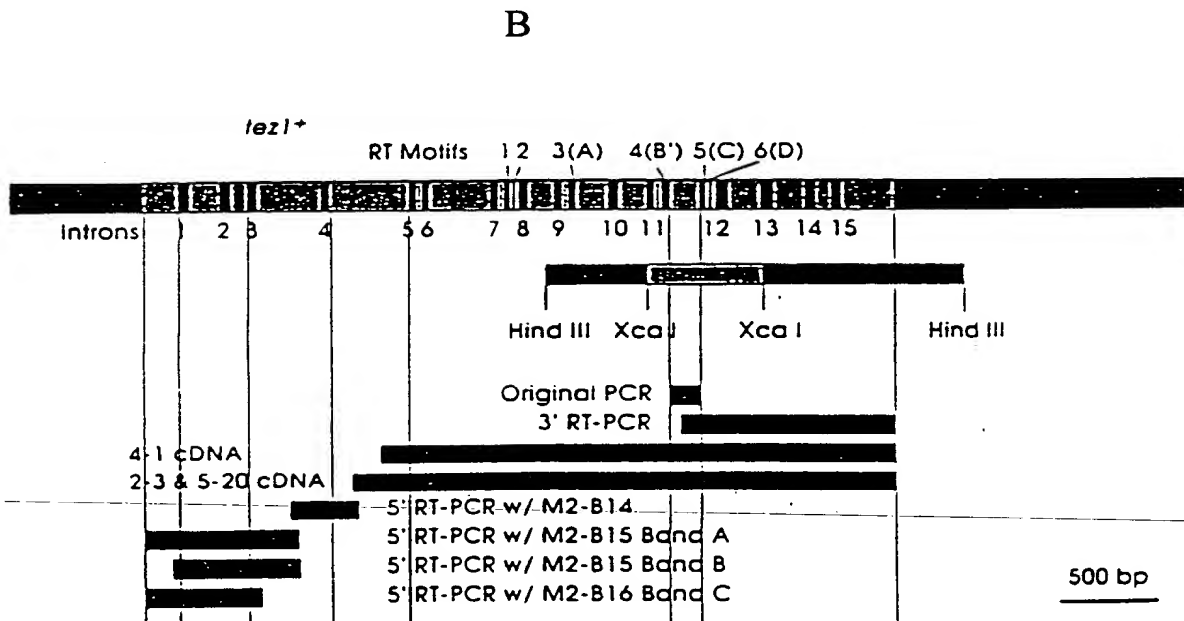
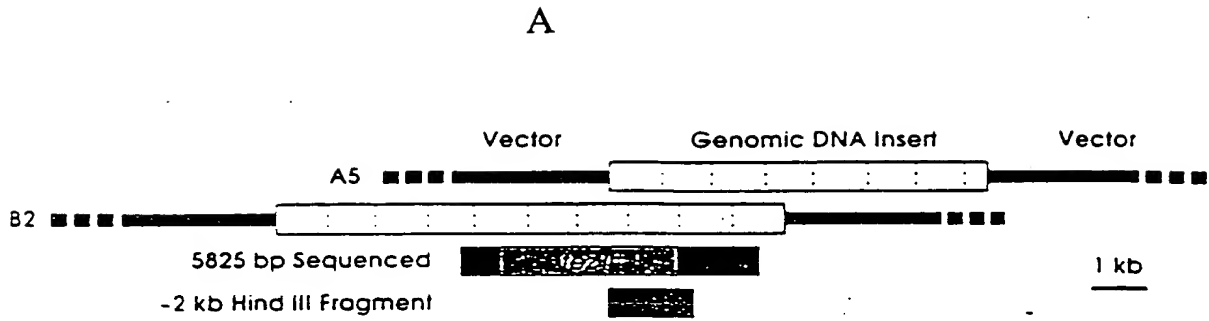
Figure 54

S-1: FFY VTE TTF QKN RLF FYR KSV WSK  
S-2: RQH LKR VQL RDV SEA EVR QHR EA  
S-3: ART FRR EKR AER LTS RVK ALF SVL NYE

A-1: AKF LHW LMS VYV VEL LRS FFY VTE TTF Q  
A-2: LFF YRK SVW SKL QSI GIR QHL KRV QLR DVS  
A-3: PAL LTS RLR FIP KPD GLR PIV NMD YVV

66207E" ED52E460

Figure 55



04432503.10299

Figure 56

Poly 4

	t		t		c			
	t	a	a	g	c	c	t	c g
5'-	cag	acc	aaa	gga	att	cca	taa	gg -3'
	Q	T	K	G	I	P	Q	G

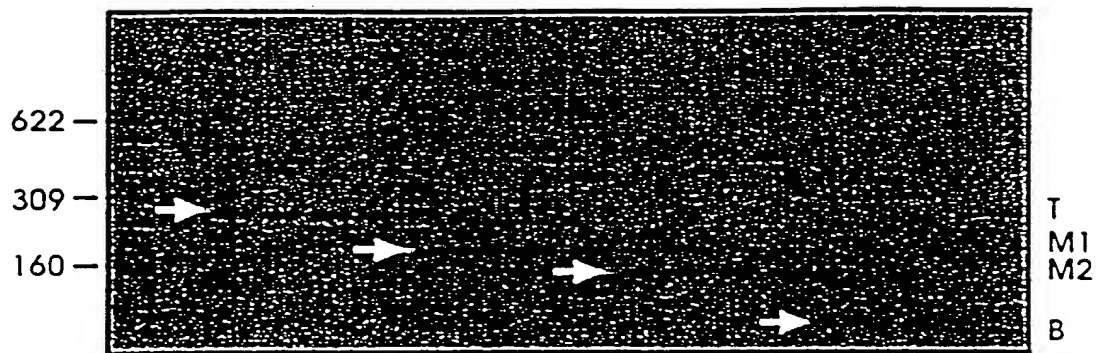
4 (B')

5 (c')

	D	D	Y	L	L	I	T	
3'-	ctg	ctg	atg	gag	gag	tag	tgg	-5'
	a	a	a	a	a	a	a	
			t	t		t	t	
						c	c	
						<u>Poly 1</u>		

00433503-10000

Figure 57



Motif B' (4)  
QTKGIPQG

Motif C (5)  
DDYLLIT

09432503 " 110299  
662011" 20523460

Figure 58

# PCR Product M2 showed Reasonable Match with Other Telomerase Proteins

Ot	LCVSYILSSFFYYANLEENALQFLRKESMDPEKPETNLLMRLT
Ea_p123	KGIPQGLCVSSILSSFFYYATLEESSLGFLRDESMNPENPNVNLLMRLTDDYLLIT
Sp_M2	SILSSFLCHFYMEDLIDEYLSFTKKK-----GSVLLRVV
Sc_p103	DGLFQGSSLSAPIVDLVYDDLLEFYSEFKASPS-----QDTLILKLADDFLIIS
	. * . * . * . . . . .

Q K V G I P Q G  
 caa aaa gtt ggt atc cct cag gg..... <---Actual Genomic Sequence.

## Poly 4

t t c  
 t a g c c t c g  
 cag acc aaa gga att cca taa gg ---->

ag acc aaa gga att cca tca ggC TCA ATT CTG TCA TCT TTT TTG TGT CAT TTC TAT ATG  
 tc tgg ttt cct taa ggt agt ccG AGT TAA GAC AGT AGA AAA AAC ACA GTA AAG ATA TAC

K G : P S G S I L S S F L C H F Y M

GAA GAT TTG ATT GAT GAA TAC CTA TCG TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA  
 CTT CTA AAC TAA CTA CTT ATG GAT AGC AAA TGC TTT TTC TTT CCT AGT CAC AAC AAT GCT

E D L I D E Y L S F T K K K G S V L L R

~~GTA-GTC-gac-gac-tac-ctc-ctc-acc-~~  
 CAT CAG ctg ctg atg gag gag tag tgg

V V D D Y L L I T

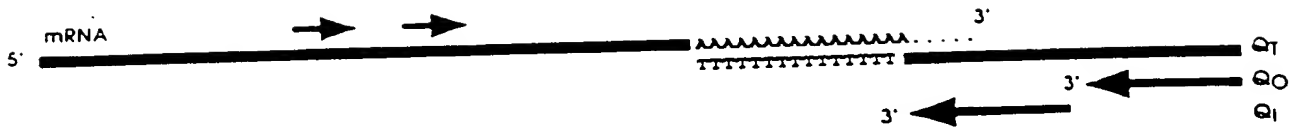
<---- ctg ctg atg gag gag tag tgg  
 a a a a a a a a  
 t t t t  
 c c

## Poly 1

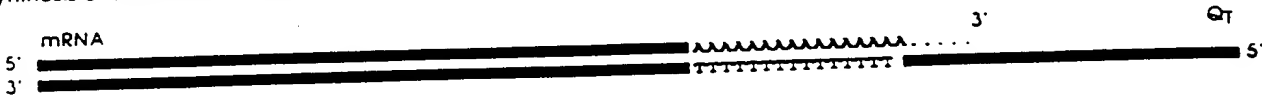
.....gac gat ttc ctc ttt ata aca..... <---Actual Genomic Sequence.  
 D D F L F I T

Figure 59

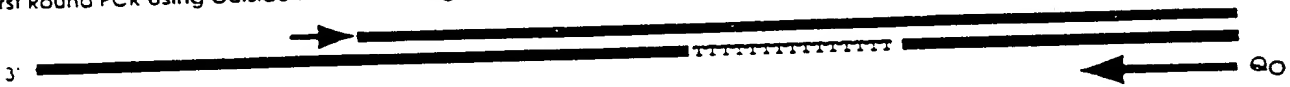
### 3' RT PCR Strategy



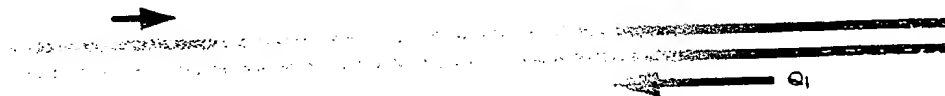
1. Synthesis of cDNA with Q<sub>1</sub> Primer.



2. First Round PCR Using Outside Primer and Q<sub>0</sub> Primer.



3. Second Round PCR Using Inside Primer and Q<sub>I</sub> Primer.



4. Sequence Second Round PCR Products Using Inside Primer or Q<sub>I</sub> Primer.



Figure 60

A

-Size Selected Libraries from P. Nurese

- 3 - 4 kb
- 5 - 6 kb
- 7 - 8 kb
- 11 - 12 kb

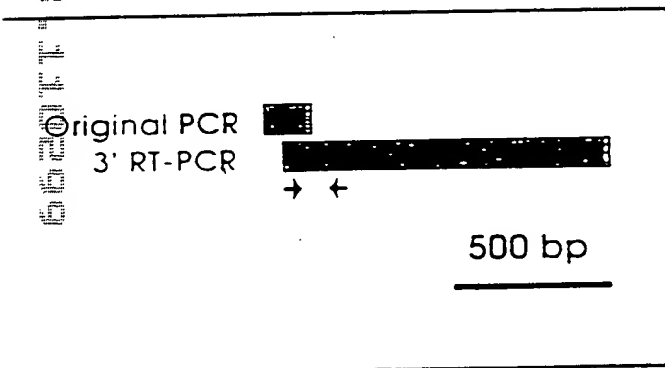
-Libraries from J.A. Wise

- Sau 3a Partial Digest
- Hind III Partial Digest

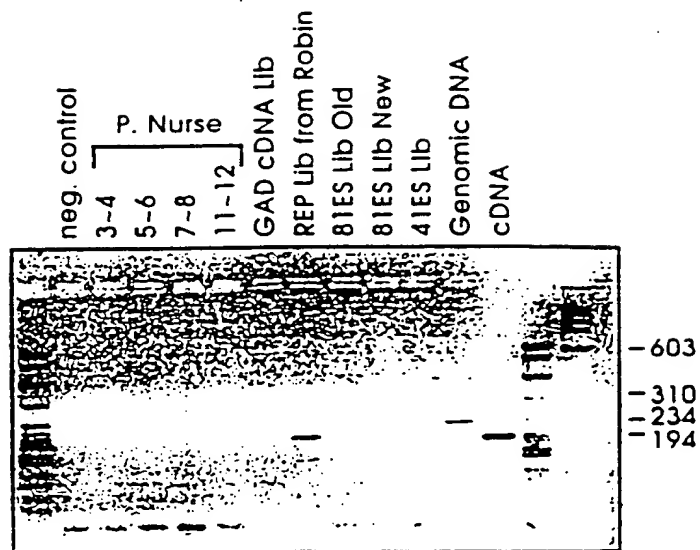
cDNA Libraries

- GAD (Gal Activation Domain) Library
- REP Library from R. Allshire
- REP81ES Library (old)
- REP81ES Library (new)
- REP41ES Library

B



C



D

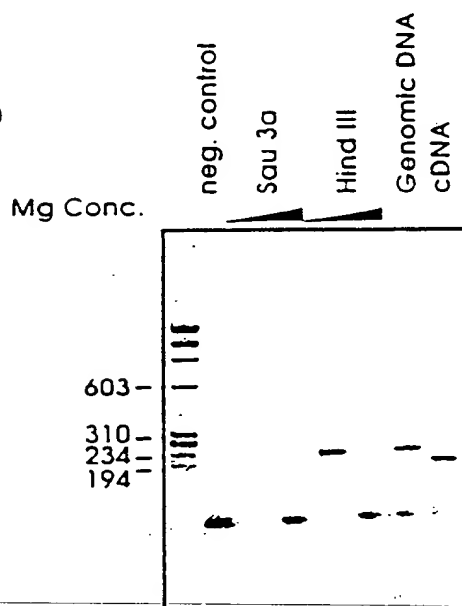
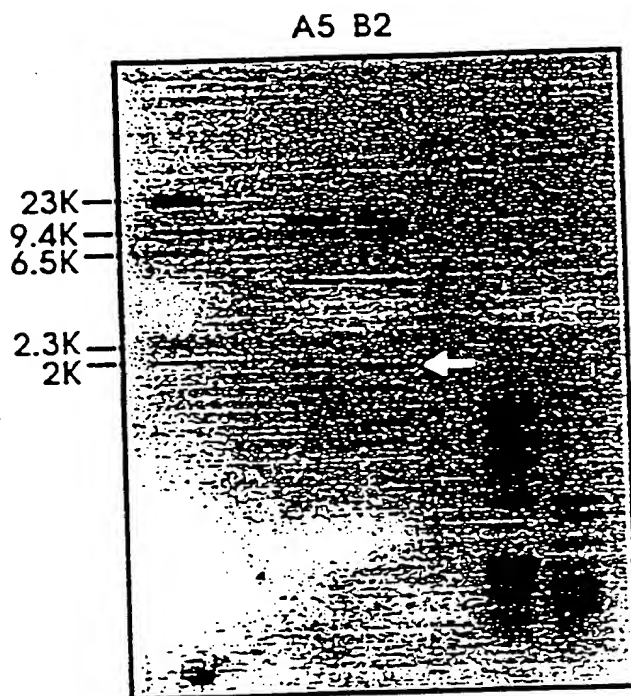


Figure 61

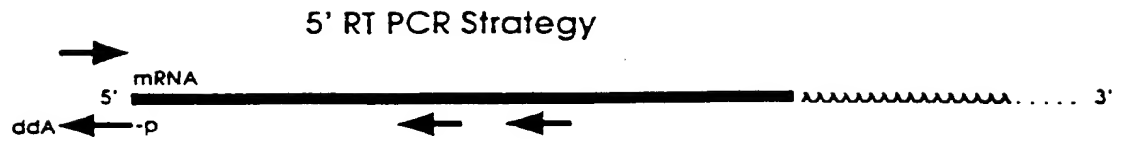


Hind III Digested Positive Genomic Clones

0943503-11029  
6620T-0522460



Figure 62



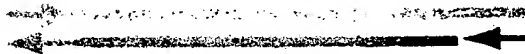
1. Synthesis of cDNA with Specific Downstream Primer.



2. Ligate Oligo with 5'-P and blocked 3' to cDNA using T4 RNA Ligase.



3. First Round PCR



4. Second Round PCR

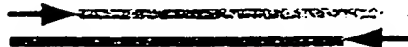


Figure 63

# Alignment of RT Domains from Telomerase Catalytic Subunits.

0543503.14099

```

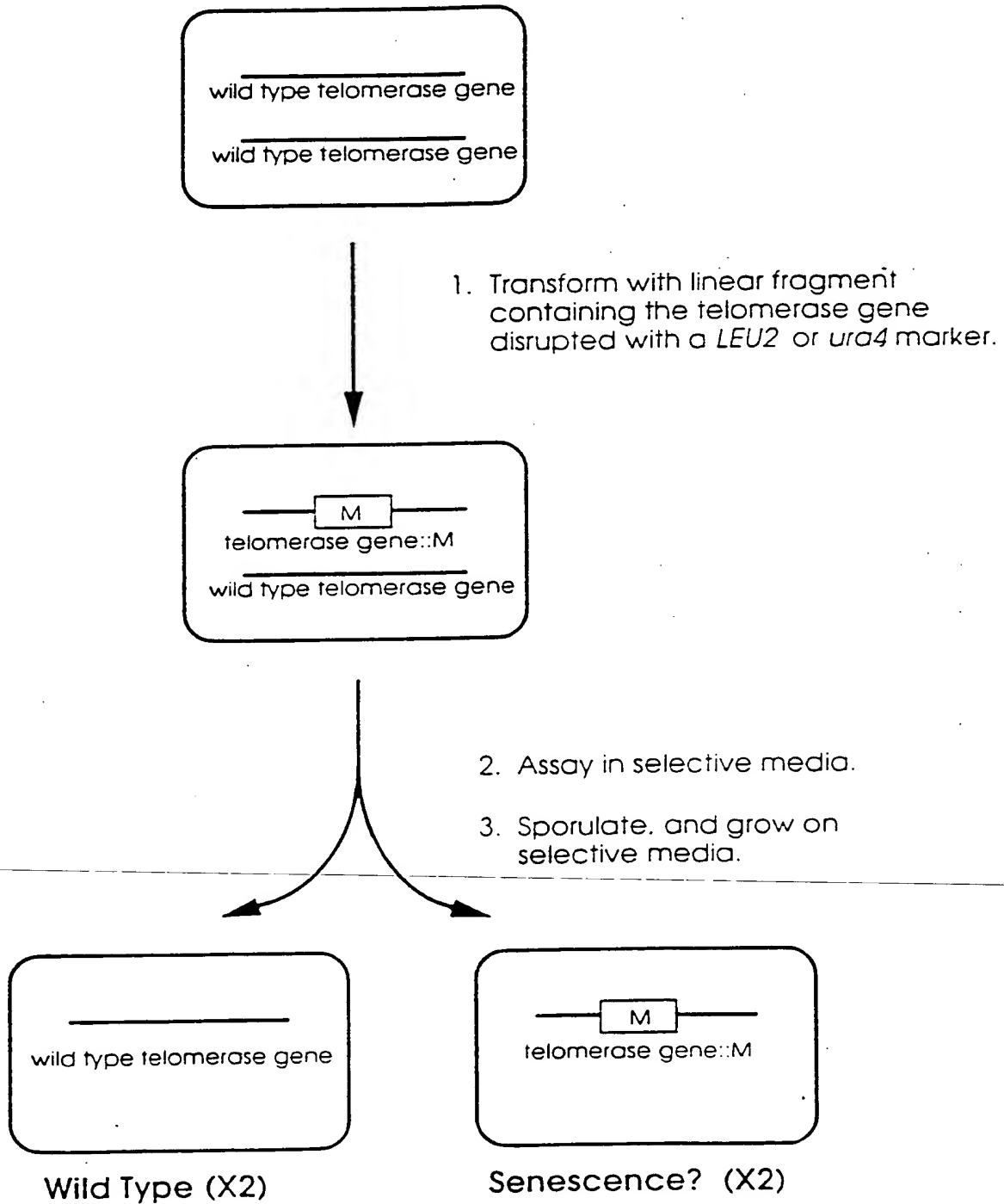
                                Motif O
S.p. Tez1p (429). WLYNSFIIPILQSFFYITESDDLNRNTVYFRKDIW ... (35)...
S.c. Est2p (366). WLFRQLIPKIIQTFFYCTEISSTVT-IVYFRHDTW ... (35)...
E.a. p123 (441). WIFEDLVVSLIRCFFYVTEQQKSYSKTYYYRKNIW ... (35)...
      *          *** **          * * *
      Motif 1      Motif 2      K
      p hh h K      hR h      R
S.p. Tez1p AVIRLLPKK--NTFRLITN-LRKRF ... (61)...
S.c. Est2p SKMRIIPKKSNNEFRIIAIPCRGAD ... (62)...
E.a. p123 GGLRLIPKK--TTFRPIMTFNKKIV ... (61)...
      *   ***   ** *
      Motif 3(A) AF
      h hDh GY h
S.p. Tez1p KKYFVRIDIKSCYDRIKQDLMFRIVK ... (89)...
S.c. Est2p ELYFMKFDVNSCYDSIPRMECMFILK ... (75)...
E.a. p123 KLFATMDIEKCYDSVNREKLSTFLK ... (107)...
      *   *   ***   *
      Motif 4(B')
      hPQG pP hh h
S.p. Tez1p YLQKVGIPQGSILSSFLCHFYMEDLIDEYLSF ... (6)...
S.c. Est2p YIREDGLFQGSSLSAPIVDLVYDDLLEFYSEF ... (8)...
E.a. p123 YKQTKGIPQGLCVSSILSSFYYATLEESSLGF ... (14)...
      *   *   *   *   *
      Y Motif 5(C)                      Motif 6(D)
      h F DDhhh                      Gh h cK h
S.p. Tez1p VLLRVVDDFLFITVNKKDAKKFLNLSLRGFEKHNFSTSLEKTVINFENS . (205)
S.c. Est2p LILKLADDFLIISTDQQQVINIKKLAMGGFQKYNAKANRDKILAVSSQS . (173)
E.a. p123 LLMRLTDDYLLITTQENNAVLFIKLINVSRENGEFKFMKKLQTSFPLS . (209)
      ** * *                      *

```

[illegible][illegible][illegible]

Figure 65

## Disruption strategy for the putative telomerase genes.



(These cells will show a senescence phenotype if the disrupted gene encodes a telomerase subunit.)

Figure 66

# An Example of Confirmation of *tez1* disruption By PCR

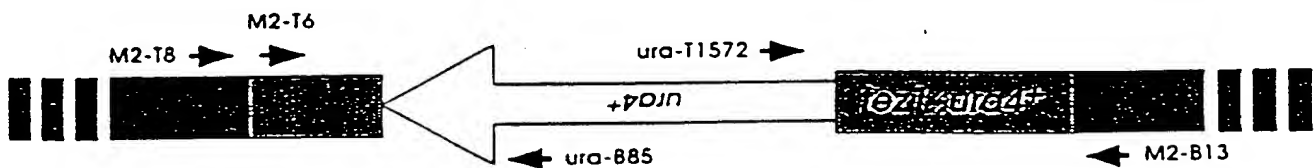
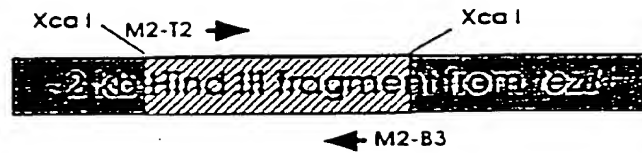
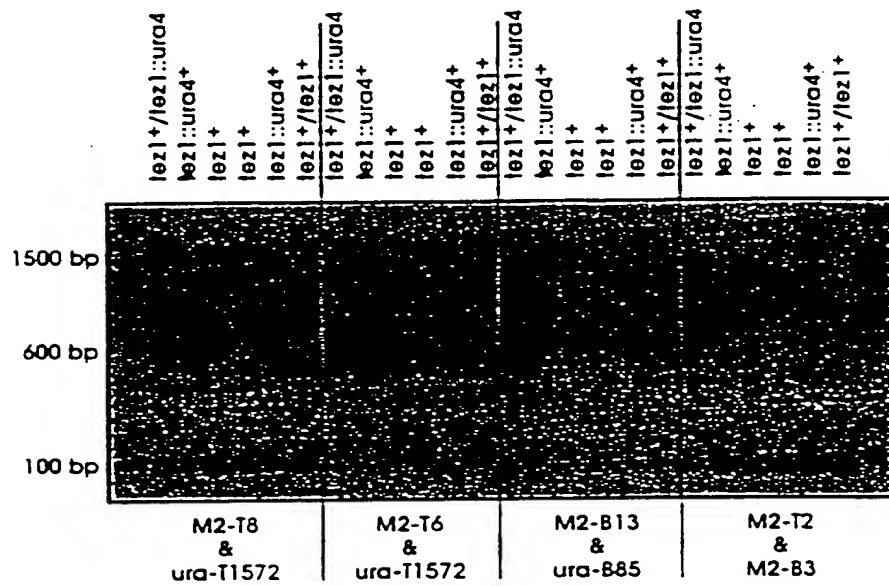
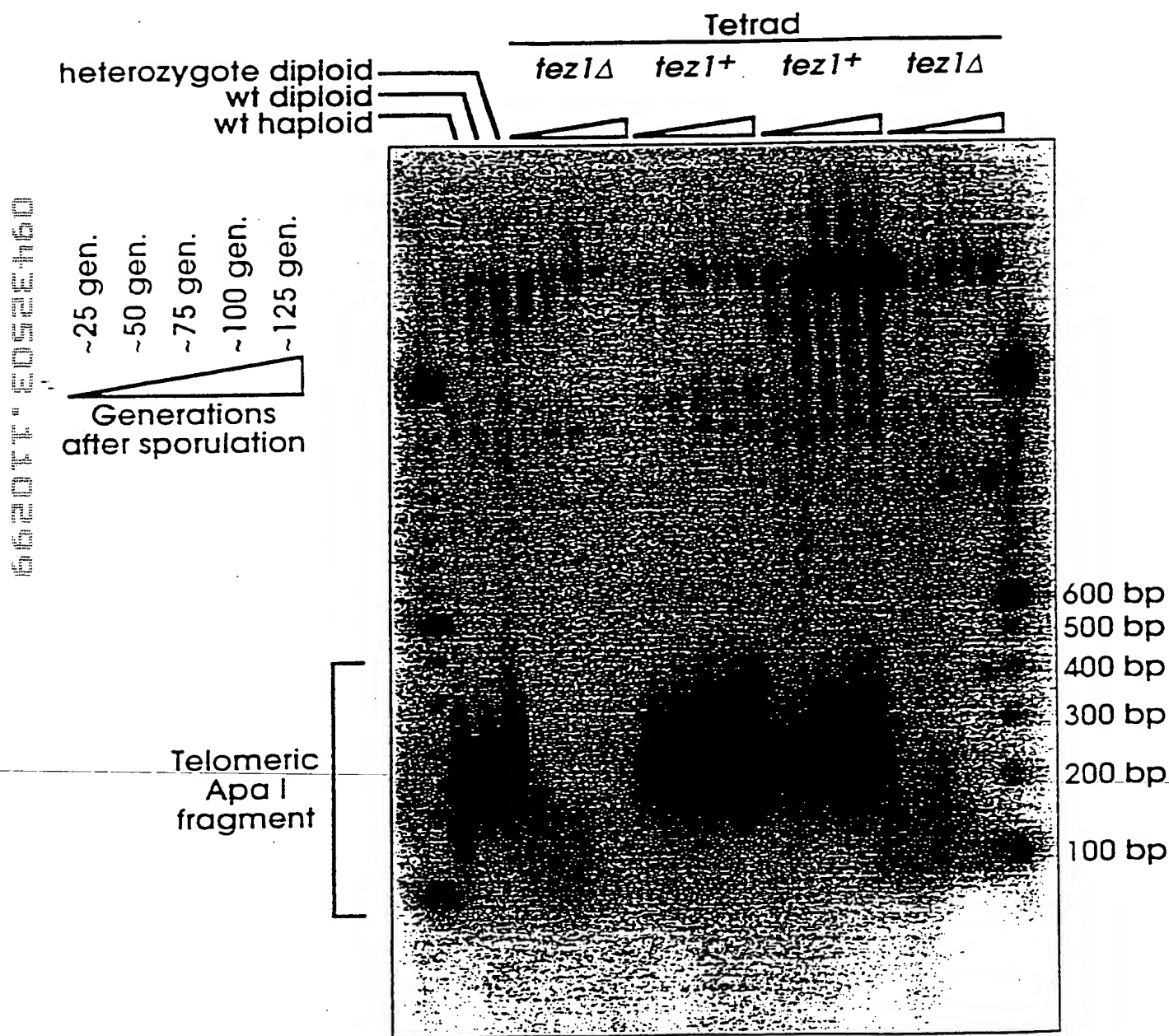


Figure 67

# *Tez1* disruption causes progressive shortening of telomeres in *S. pombe*



						1	met	ser	val	tyr	val	val	glu	leu	leu
GCCAAGTTCCTGCACTGGCTG						ATG	AGT	GTG	TAC	GTC	GTC	GAG	CTG	CTC	
10						20									
arg	ser	phe	phe	tyr	val	thr	glu	thr	thr	phe	gln	lys	asn	arg	
AGG	TCT	TTC	TTT	TAT	GTC	ACG	GAG	ACC	ACG	TTT	CAA	AAG	AAC	AGG	
30						40									
leu	phe	phe	tyr	arg	lys	ser	val	trp	ser	lys	leu	gln	ser	ile	
CTC	TTT	TTC	TAC	CGG	AAG	AGT	GTC	TGG	AGC	AAG	TTG	CAA	AGC	ATT	
50						60									
gly	ile	arg	gln	his	leu	lys	arg	val	gln	leu	arg	glu	leu	ser	
GGA	ATC	AGA	CAG	CAC	TTG	AAG	AGG	GTG	CAG	CTG	CGG	GAG	CTG	TCG	
70						80									
glu	ala	glu	val	arg	gln	his	arg	glu	ala	arg	pro	ala	leu	leu	
GAA	GCA	GAG	GTC	AGG	CAG	CAT	CGG	GAA	GCC	AGG	CCC	GCC	CTG	CTG	
90						100									
thr	ser	arg	leu	arg	phe	ile	pro	lys	pro	asp	gly	leu	arg	pro	
ACG	TCC	AGA	CTC	CGC	TTC	ATC	CCC	AAG	CCT	GAC	GGG	CTG	CGG	CCG	
110						120									
ile	val	asn	met	asp	tyr	val	val	gly	ala	arg	thr	phe	arg	arg	
ATT	GTG	AAC	ATG	GAC	TAC	GTC	GTG	GGA	GCC	AGA	ACG	TTC	CGC	AGA	
130						140									
glu	lys		ala	glu	arg	leu	thr	ser	arg	val	lys	ala	leu	phe	
GAA	AAG	ARG	GCC	GAG	CGT	CTC	ACC	TCG	AGG	GTG	AAG	GCA	CTG	TTC	
150						160									
ser	val	leu	asn	tyr	glu	arg	ala	arg	arg	pro	gly	leu	leu	gly	
AGC	GTG	CTC	AAC	TAC	GAG	CGG	GCG	CGG	CGC	CCC	GGC	CTC	CTG	GGC	
170						180									
ala	ser	val	leu	gly	leu	asp	asp	ile	his	arg	ala	trp	arg	thr	
GCC	TCT	GTG	CTG	GGC	CTG	GAC	GAT	ATC	CAC	AGG	GCC	TGG	CGC	ACC	
190						200									
phe	val	leu	arg	val	arg	ala	gln	asp	pro	pro	pro	glu	leu	tyr	
TTC	GTG	CTG	CGT	GTG	CGG	GCC	CAG	GAC	CCG	CCG	CCT	GAG	CTG	TAC	
210						220									
phe	val	lys	val	asp	val	thr	gly	ala	tyr	asp	thr	ile	pro	gln	
TTT	GTC	AAG	GTG	GAT	GTG	ACG	GGC	GCG	TAC	GAC	ACC	ATC	CCC	CAG	
230						240									
asp	arg	leu	thr	glu	val	ile	ala	ser	ile	ile	lys	pro	gln	asn	
GAC	AGG	CTC	ACG	GAG	GTC	ATC	GCC	AGC	ATC	ATC	AAA	CCC	CAG	AAC	

Figure 68 (cont.)

190 thr tyr cys val arg arg tyr ala val val 200 gln lys ala ala met  
 ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC ATG  
 210  
 gly thr ser ala arg pro ser arg ala thr ser tyr val gln cys  
 GGC ACG TCC GCA AGG CCT TCA AGA GCC ACG TCC TAC GTC CAG TGC  
 220 230  
 gln gly ile pro gln gly ser ile leu ser thr leu leu cys ser  
 CAG GGG ATC CCG CAG GGC TCC ATC CTC TCC ACG CTG CTC TGC AGC  
 240  
 leu cys tyr gly asp met glu asn lys leu phe ala gly ile arg  
 CTG TGC TAC GGC GAC ATG GAG AAC AAG CTG TTT GCG GGG ATT CGG  
 250 260  
 arg asp gly leu leu leu arg leu val asp asp phe leu leu val  
 CGG GAC GGG CTG CTC CTG CGT TTG GTG GAT GAT TTC TTG TTG GTG  
 270  
 thr pro his leu thr his ala lys thr phe leu arg thr leu val  
 ACA CCT CAC CTC ACC CAC GCG AAA ACC TTC ACC ACC CTG GTC  
 280 290  
 arg gly val pro glu tyr gly cys val val asn leu arg lys thr  
 CGA GGT GTC CCT GAG TAT GGC TGC GTG GTG AAC TTG CCG AAG ACA  
 300  
 val val asn phe pro val glu asp glu ala leu gly gly thr ala  
 GTG GTG AAC TTC CCT GTA GAA GAC GAG GCC CTG GGT GGC ACG GCT  
 310 320  
 phe val gln met pro ala his gly leu phe pro trp cys gly leu  
 TTT GTT CAG ATG CCG GCC CAC GGC CTA TTC CCC TGG TGC GGC CTG  
 330  
 leu leu asp thr arg thr leu glu val gln ser asp tyr ser ser  
 CTG CTG GAT ACC CGG ACC CTG GAG GTG CAG AGC GAC TAC TCC AGC  
 340 350  
 tyr ala arg thr ser ile arg ala ser leu thr phe asn arg gly  
 TAT GCC CGG ACC TCC ATC AGA GCC AGT CTC ACC TTC AAC CGC GGC  
 360  
 phe lys ala gly arg asn met arg arg lys leu phe gly val leu  
 TTC AAG GCT GGG AGG AAC ATG CGT CGC AAA CTC TTT GGG GTC TTG  
 370 380  
 arg leu lys cys his ser leu phe leu asp leu gln val asn ser  
 CGG CTG AAG TGT CAC AGC CTG TTT CTG GAT TTG CAG GTG AAC AGC

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Figure 68 (cont.)

390  
leu gln thr val cys thr asn ile tyr lys ile leu leu leu gln  
CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG CTG CAG

400 410  
ala tyr arg phe his ala cys val leu gln leu pro phe his gln  
GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT CAT CAG

420  
gln val trp lys asn pro his phe ser cys ala ser ser leu thr  
CAA GTT TGG AAG AAC CCA CAT TTT TCC TGC GCG TCA TCT CTG ACA

430 440  
arg leu pro leu leu leu his pro glu ser gln glu arg arg asp  
CGG CTC CCT CTG CTA CTC CAT CCT GAA AGC CAA GAA CGC AGG GAT

450  
val ala gly gly gln gly arg arg arg pro ser ala leu arg gly  
GTC GCT GGG GGC CAA GGG CGC CGC CGG CCC TCT GCC CTC CGA GGC

460 470  
arg ala val ala val pro pro ser ile pro ala gln ala asp ser  
CGT GCA GTG GCT GTG CCA CCA AGC ATT CCT GCT CAA GCT GAC TCG

480  
thr pro cys his leu arg ala thr pro gly val thr gln asp ser  
ACA CCG TGT CAC CTA CGT GCC ACT CCT GGG GTC ACT CAG GAC AGC

490 500  
pro asp ala ala glu ser glu ala pro gly asp asp ala asp cys  
CCA GAC GCA GCT GAG TCG GAA GCT CCC GGG GAC GAC GCT GAC TGC

510  
pro gly gly arg ser gln pro gly thr ala leu arg leu gln asp  
CCT GGA GGC CGC AGC CAA CCC GGC ACT GCC CTC AGA CTT CAA GAC

520 530  
his pro gly leu met ala thr arg pro gln pro gly arg glu gln  
CAT CCT GGA CTG ATG GCC ACC CGC CCA CAG CCA GGC CGA GAG CAG

540  
thr pro ala ala leu ser arg arg ala tyr thr ser gln gly gly  
ACA CCA GCA GCC CTG TCA CGC CGG GCT TAT ACG TCC CAG GGA GGG

550 560  
arg gly gly pro his pro gly leu his arg trp glu ser glu ala  
AGG GGC GGC CCA CAC CCA GGC CTG CAC CGC TGG GAG TCT GAG GCC

564  
OP  
TGA GTGAGTGT TTTGGCCGAGGCCTGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGC  
CTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTCCAGCACACCTGCGTTTTCACTTCCCCAC

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Figure 68 (cont.)

AGGCTGGCGTTCGGTCCACCCCAGGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCACT  
CCCCACATAGGAATAGTCCATCCCCAGATTTCGCCATTGTTACCCCTTCGCCCTGCCTTCC  
TTTGCCCTTCACCCCCACCATTTCAGGTGGAGACCCTGAGAAGGACCCTGGGAGCTTTGGG  
AATTTGGAGTGACCAAAGGTGTGCCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGG  
GTCCCTGTGGGTCAAATTGGGGGGAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTT  
TTTCAGTTTTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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Figure 69

Motif -1  
 Ep p123 ...LVVSLIRCFFYVTEQQKSYSKT...  
 Sp Tez1 ...FIIPILQSFFYITESDLRNRT...  
 Sc Est2 ...LIPKIIQTFFYCTEISSTVTIV...  
 Hs TCP1 ...YVVELLRSFYVTETTFQKNRL...  
 consensus FFY TE

Motif 0  
 Ep p123 ...KSLGFAPGKRLRLIPKKT--TFRPIMTFNKKIV...  
 Sp Tez1 ...QKTTLPFAVIRLLPKKN--TFRLLITNLRKRFL...  
 Sc Est2 ...TLNFNHSMRIIPKKSNNFRIIAIPCRGAD...  
 Hs TCP1 ...ARPALLTSRLRFIPKPD--GLRPIVNMDYVVG...  
 consensus R PK RI

Motif A  
 Ep p123 ...PKLFFATMDIEKCYDSVNREKLSTFLK...  
 Sp Tez1 ...RKKYFVRIDIKSCYDRIKQDLMFRIVK...  
 Sc Est2 ...PELYFMKFDVKSCYDSIPRMECMRILK...  
 Hs TCP1 ...PELYFVKVDVTGAYDTIPQDRLTEVIA...//...  
 consensus F D YD

Motif B  
 Ep p123 ...NGKFYKQTKGIPQGLCVSSILSSFYYA...  
 Sp Tez1 ...GNSQYLQKVGIPQGSILSSFLCHFYME...  
 Sc Est2 ...EDKCYIREDGLFQGSSLSAPIVDLVYD...  
 Hs TCP1 ...RATSYVQCQGIPQGSILSTLLCSLCYG...  
 consensus G QG S

Motif C  
 Ep p123 ...VDDFLFITVNKKD...  
 Sc Est2 ...SQDTLILKLADDFLIISTDQQQ...  
 Hs TCP1 ...RRDGLLLRLVDDFLLVTPHLTH...  
 consensus DD L

Motif D  
 Ep p123 ...NVSRENGFKFNMKKL...  
 Sp Tez1 ...LNLSLRGFEEKHNFST...  
 Sc Est2 ...KKLAMGGFQKYNKA...  
 Hs TCP1 ...LRTLVRGVPEYGCVV...  
 consensus G

09432503 110259

Figure 70

55207T "E052E460

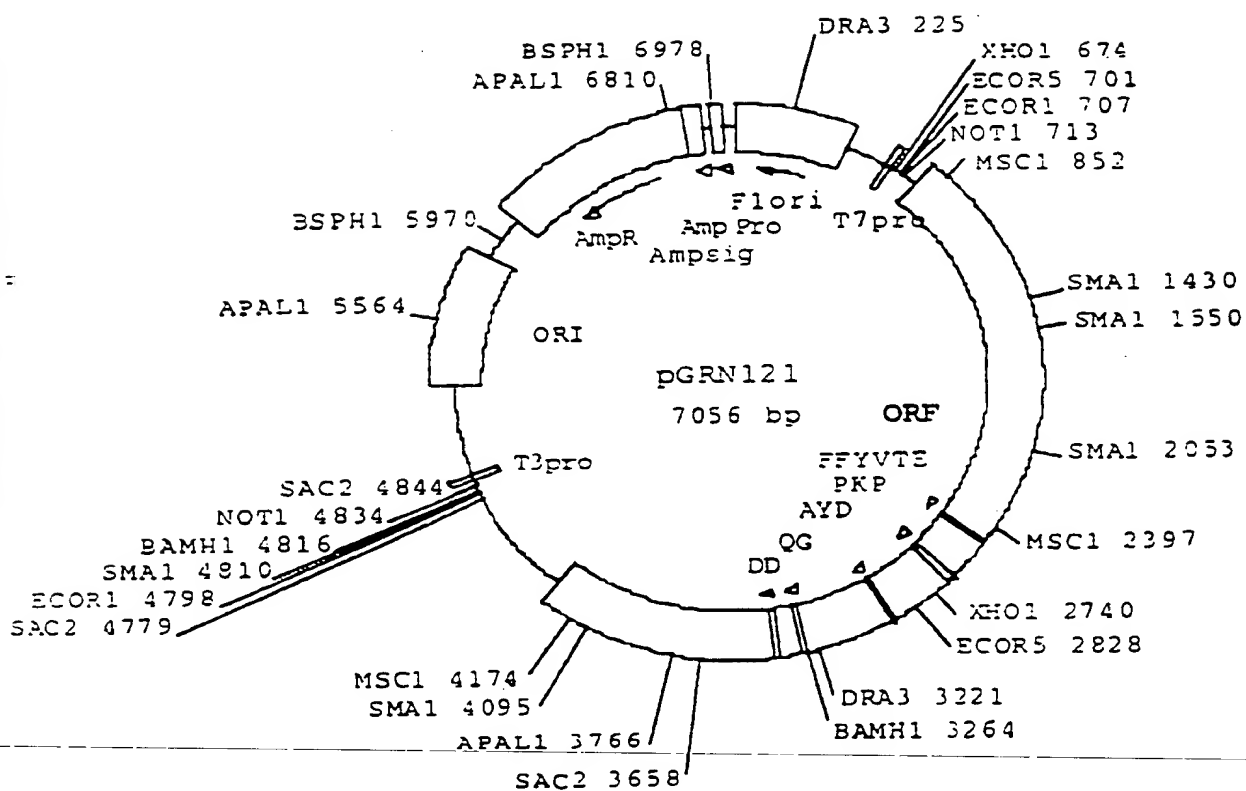


Figure 71

1 GCAGCGCTGC GTCCTGCTGC GCACGTGGGA AGCCCTGGCC CCGGCCACCC  
 51 CCGCGATGCC GCGCGCTCCC CGCTGCCGAG CCGTGCGCTC CCTGCTGCGC  
 101 AGCCACTACC GCGAGGTGCT GCCGCTGGCC ACGTTCGTGC GGCGCCTGGG  
 151 GCCCCAGGGC TGGCGGCTGG TGCAGCGCGG GGACCCGGCG GCTTTCCGCG  
 201 CGNTGGTGGC CCANTGCNTG GTGTGCGTGC CCTGGGANGN ANGGCNGCCC  
 251 CCCGCCGCCC CCTCCTTCCG CCAGGTGTCC TGCCTGAANG ANCTGGTGGC  
 301 CCGAGTGCTG CANANGCTGT GCGANCGCGG CGCGAANAAC GTGCTGGCCT  
 351 TCGGCTTCGC GCTGCTGGAC GGGGCCCGCG GGGGCCCCCC CGAGGCCTTC  
 401 ACCACCAGCG TGCGCAGCTA CCTGCCCAAC ACGGTGACCG ACGCACTGCG  
 451 GGGGAGCGGG GCGTGGGGGC TGCTGCTGCG CCGCGTGGGC GACGACGTGC  
 501 TGGTTACCT GCTGGCACGC TGC GCGNTNT TTGTGCTGGT GGN'TCCAGC  
 551 TGC GCCTACC ANGTGTGCGG GCCGCCGCTG TACCAGCTCG GCGCTGCNAC  
 601 TCAGGCCCGG CCCCCGCCAC ACGCTANTGG ACCCGAANGC GTCTGGGATC  
 651 CAACGGGCCT GGAACCATAG CGTCAGGGAG GCCGGGGTCC CCCTGGGCTG  
 701 CCAGCCCCGG GTGCGAGGAG GCGCGGGGGC AGTGCCAGCC GAAGTCTGCC  
 751 GTTGCCCAAG AGGCCAGGC GTGGCGCTGC CCCTGAGCCG GAGCGGACCG  
 801 CCGTTGGGCA GGGGTCCTGG GCCACCCGG GCAGGACGCC TGGACCGAGT  
 851 GACCGTGGTT TCTGTGTGGT GTCACCTGCC AGACCCGCCG AAGAAGCCAC  
 901 CTCTTTGGAG GGTGCGCTCT CTGGCACGCG CCACTCCAC CCATCCGTGG  
 951 GCCGCCAGCA CCACGCGGGC CCCCCATCCA CATCGCGGCC ACCACGTCCT  
 1001 GGGACACGCC TTGTCCCCCG GTGTACGCCG AGACCAAGCA CTTCTCTAC  
 1051 TCCTCAGGCG ACAAGNACAC TGCNCCCTC CTTCTACTC AATATATCTG  
 1101 AGGCCAGCC TGA CTGGCGT TCGGGAGGTT CGTGGAGACA NTCTTTCTGG  
 1151 TTCCAGGCCT TGGATGCCAG GATTCCCCGC AGGTTGCCCC GCCTGCCCCA  
 1201 GCGNTACTGG CAAATGCGGC CCCTGTTTCT GGAGCTGCTT GGAACACG  
 1251 CGCAGTGCCC CTACGGGGTG TTCCTCAAGA CGCACTGCCC GCTGCGAGCT  
 1301 GCGGTCACCC CAGCAGCCGG TGTCTGTGCC CGGGAGAAGC CCCAGGGCTC  
 1351 TGTGGCGGCC CCCGAGGAGG AGGAACACAG ACCCCCGTCG CCTGGTGCAG  
 1401 CTGCTCCGCC AGCACAGCAG CCCCTGGCAG GTGTACGGCT TCGTGCGGGC  
 1451 CTGCCTGCGC CGGCTGGTGC CCCCAGGCCT CTGGGGCTCC AGGCACAACG  
 1501 AACGCCGCTT CCTCAGGAAC ACCAAGAAGT TCATCTCCCT GGGGAAGCAT  
 1551 GCCAAGCTCT CGCTGCAGGA GCTGACGTGG AAGATGAGCG TCGGGGACTG  
 1601 CGCTTGCTG CGCAGGAGCC CAGGGGTTGG CTGTGTTCCG GCCGCAGAGC  
 1651 ACCGTCTGCG TGAGGAGATC CTGGCCAAGT TCCTGCACTG GCTGATGAGT  
 1701 GTGTACGTCG TCGAGCTGCT CAGGTCTTTC TTTTATGTCA CGGAGACCAC  
 1751 GTTTCAAAAG AACAGGCTCT TTTTCTACCG GAAGAGTGTC TGGAGCAAGT  
 1801 TGCAAAGCAT TGAATCAGA CAGCACTTGA AGAGGGTGCA GCTGCGGGAG  
 1851 CTGTCCGAAG CAGAGGTCAG GCAGCATCGG GAAGCCAGGC CCGCCCTGCT  
 1901 GACGTCCAGA CTCCGCTTCA TCCCAAGCC TGACGGGCTG CGGCCGATTG  
 1951 TGAACATGGA CTACGTCGTG GGAGCCAGAA CGTTCCGCAG AGAAAAGAGG  
 2001 GCCGAGCGTC TCACCTCGAG GGTGAAGGCA CTGTTACGCG TGCTCAACTA  
 2051 CGAGCGGGCG CGGCGCCCCG GCCTCCTGGG CGCCTCTGTG CTGGGCCTGG  
 2101 ACGATATCCA CAGGGCCTGG CGCACCTTCG TGCTGCGTGT GCGGGCCAG  
 2151 GACCCGCCGC CTGAGCTGTA CTTTGTCAAG GTGGATGTGA CGGGCGCGTA  
 2201 CGACACCATC CCCCAGGACA GGCTCACGGA GGTCATCGCC AGCATCATCA  
 2251 AACCCAGAA CACGTACTGC GTGCGTCGGT ATGCCGTGGT CCAGAAGGCC

Figure 71 (cont.)

2301 GCCCATGGGC ACGTCCGCAA GGCCTTCAAG AGCCACGTCT CTACCTTGAC  
2351 AGACCTCCAG CCGTACATGC GACAGTTCGT GGCTCACCTG CAGGANAACA  
2401 GCCCGCTGAG GGATGCCGTC GTCATCGAGC AGAGCTCCTC CCTGAATGAG  
2451 GCCAGCAGTG GCCTCTTCGA CGTCTTCCTA CGCTTCATGT GCCACCACGC  
2501 CGTGCGCATC AGGGGCAAGT CCTACGTCCA GTGCCAGGGG ATCCCGCAGG  
2551 GCTCCATCCT CTCCACGCTG CTCTGCAGCC TGTGCTACGG CGACATGGAG  
2601 AACAAGCTGT TTGCGGGGAT TCGGCGGGAC GGGCTGCTCC TGC GTTTGGT  
2651 GGATGATTTT TTGTTGGTGA CACCTCACCT CACCCACGCG AAAACCTTCC  
2701 TCAGGACCCT GGTCCGAGGT GTCCCTGAGT ATGGCTGCGT GGTGAACTTG  
2751 CGGAAGACAG TGGTGAACCT CCCTGTAGAA GACGAGGCCC TGGGTGGCAC  
2801 GGCTTTTGTT CAGATGCCGG CCCACGGCCT ATCCCTCTGG TCGGGCCTGC  
2851 TGCTGGATAC CCGGACCCTG GAGGTGCAGA GCGACTACTC CAGCTATGCC  
2901 CGGACCTCCA TCAGAGCCAG TCTCACCTTC AACCGCGGCT TCAAGGCTGG  
2951 GAGGAACATG CGTCGCAAAC TCTTTGGGGT CTTGCGGCTG AAGTGTCACA  
3001 GCCTGTTTCT GGATTTGCAG GTGAACAGCC TCCAGACGGT GTGCACCAAC  
3051 ATCTACAAGA TCCTCCTGCT GCAGGCGTAC AGGTTTCACG CATGTGTGCT  
3101 GCAGCTCCCA TTTCATCAGC AAGTTTGGA GAACCCCA TTTTCTCTGC  
3151 GCGTCATCTC TGACACGGCC TCCCTCTGCT ACTCCATCCT GAAAGCCAAG  
3201 AACGCAGGGA TGTCGCTGGG GGCCAAGGGC GCCGCCGGCC CTCTGCCCTC  
3251 CGAGGCCGTG CAGTGGCTGT GCCACCAAGC ATTCCTGCTC AAGCTGACTC  
3301 GACACCGTGT CACCTACGTG CCACTCCTGG GGTCACTCAG GACAGCCCAG  
3351 ACGCAGCTGA GTCGGAAGCT CCCGGGGACG ACGCTGACTG CCCTGGAGGC  
3401 CGCAGCCAAC CCGGCACTGC CCTCAGACTT CAAGACCATC CTGGACTGAT  
3451 GGCCACCCGC CCACAGCCAG GCCGAGAGCA GACACCAGCA GCCCTGTCAC  
3501 GCCGGGCTCT ACGTCCCAGG GAGGGAGGGG CGGCCACAC CCAGGCCCGC  
3551 ACCGCTGGGA GTCTGAGGCC TGAGTGAGTG TTTGGCCGAG GCCTGCATGT  
3601 CCGGCTGAAG GCTGAGTGTC CGGCTGAGGC CTGAGCGAGT GTCCAGCCAA  
3651 GGGCTGAGTG TCCAGCACAC CTGCCGTCTT CACTTCCCCA CAGGCTGGCG  
3701 CTCGGCTCCA CCCCAGGGCC AGCTTTTCCT CACCAGGAGC CCGGCTTCCA  
3751 CTCCCCACAT AGGAATAGTC CATCCCCAGA TTCGCCATTG TTCACCCCTC  
3801 GCCCTGCCCT CTTTGCCTT CCACCCCA CATCCAGGTG GAGACCCTGA  
3851 GAAGGACCCT GGGAGCTCTG GGAATTTGGA GTGACCAAAG GTGTGCCCTG  
3901 TACACAGGCG AGGACCCTGC ACCTGGATGG GGCTCCCTGT GGGTCAAATT  
3951 GGGGGGAGGT GCTGTGGGAG TAAATACTG AATATATGAG TTTTTCAGTT  
4001 TTGAAAAAAA AAAAAAAAAA AAAAAAAAAA

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S C T G . . V C T S S S C S C L S F M S -  
 F A I A D E C V K R R A A Q V F L L C H -  
 L H W I M S V Y V V E L L R S F F Y V T -

R R P P P K R T G S F S T G R V S G A S -  
G D H V S K E Q A L F L P E E C L E Q V -  
E T T P C K N R L F F Y R K S V W S K L -

C K A L E S D S T \* R G C S C G S C R K -  
 A K H W N O T A L E E C A A A C A V C S -  
 O S T G I R O H L K R V Q L R E L S E A -

Q R E G S I G K P G P P C \* R F D S A S -  
E G Q A A S C S O A R P A D V O T P L H -  
E V E O H R E A F F A L L T S R L R F I -

S P E L T G C G R L \* T W T T S W E P E -  
P O A \* R A A A D C E H C L R R G S Q N  
P K P D G L R P I V N M D Y V V G A R T

R S A E K R C P S V S P H G \* P H C S A -  
V P Q R K E G R A S H L E G E C T V Q R  
F R R E K R A E P L T S R V K A L F S V

C S T T S G R G A P A S W A F L C W A W -  
 A O L S A G A A P H P P G R L C A G F G -  
 L N T E E A R E P G L L G A E W L G L D

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Figure 72 (cont.)

CCTAGCTCCAGTTCACCGGATGTCGGGAGGCTCTATGCTCTGCGGCTGCTGCGGCC  
 2521 ..... 2590  
 GGATGCAAGCTTACGCTCCCTTAGGCGCTCCGAGGTAGGAGAGGTGCGAGGAGCGCTGG

A P T S S A R G S R R A F S S P R C S A A -  
 D L R P V P G D P A G L H F L H A A L Q F -  
 C Y V Q C C C I P Q G S I L S T L L C S L -

TGTATACGGGACATGAGACAAGCTTTTTCGGGGATTGGGCGGACGGGCTGCTTC  
 2591 ..... 2640  
 ACACATATGCGCTGTACCTCTTCTTTCGACAAACGCTCCCTTAAGCGCGCTGCGCGAGGAGG

A C A T A T W K T S C L R C F G G T C C S -  
 D V L R R H G E Q A V C G D S A G R A A F -  
 C C Y G D H E N K L F A G I R R D G L L L -

TCGCTTTGCTGGAGATTTCTTCTTCTGCTCAGACCTCAGCTCAAGGACGCGAAAACTTCC  
 2641 ..... 2700  
 AAGCGAAACCGCTTACTAAAGAACCACTACTCTGAGCTGAGTGGGTCGCTTTTGGGAAGG

A C V W W M I S C W \* H L T S P T K K P S -  
 D A F G G \* F I V G D T S P H F R E N L P -  
 C R L V D D F L L V T P H L T H A K T F L -

TCAGGACGCTTCTGCTAGCTCTGCTCTAGCTATGCTTCTGCTGTAAGCTTGGCGAAGACAG  
 2701 ..... 2760  
 AGTCTCTGAGACCGGCTCCACAGGGACTTCATACCGACCGCACTTCAAGCGCTTCTGCTC

A S C P W S E V S L S M A A W \* T C G R Q -  
 D Q D P G P R C P \* V W L R G E L A E D S -  
 C F T L V R G V P E Y G C V V N L R K T V -

TCGTCAACTTCTCTGTAGAAGACGAGGCGCTGCGTGCACCGCTTTTCTTTCAGATCGCGG  
 2761 ..... 2820  
 ACCACTTGAGGGACATCTTCTGCTCCGGGACCGACCTGCTGAGGAGAACTTCTGCTC

A W \* T S L \* K T R F W V A K L L F R C R -  
 D G E L P C R R R C P C W H C F C S D A G -  
 C V N F P V E D E A L G G T A F V Q M P A -

CCCACGGCTATTCGCTCTGCTGCGGCTGCTGCTGCTATACCGGACGCTGCGAGCTCCAG  
 2821 ..... 2880  
 GGGTCCCGGATAAGCGGACCGCTGCGAGGAGGCTATGAGCTGCGAGCTTCAAGCTT

A P T A Y S P G A A C C W I P C P W R C R -  
 D P R P I P L V R F A A G Y P D F G G A E -  
 C H G L F P W C G L L L C T R T L E V Q S -

GCGACTACTGCACTATGCGCGGACCTGCTATCAGAGGCACTCTCAGCTTCAACCGCGCTT  
 2881 ..... 2940  
 CGCTTATGAGCTGAGTACCGGCTCTGAGGCTGCTGCTGCTGAGGAGTGGGAGTGGCGGCA

A A T T P A M P G P P S E P V S P S T A A -  
 D R L L Q L C P D L H Q S Q S H L Q P F L -  
 C D Y S E Y A R T S I R A S L T E N R G F -

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Figure 72 (cont.)

TCAAGCTGAGGAGACATGCTGCGAACTTTTTGGGTCTTGGGGCTGAAGTGTGACA  
 2941 ----- 3000  
 AGTTGAGACGCTCTCTGTACGTAAGCTTTAGAAAGCGCCAGAACGCGACTTACAGTGT  
  
 S E L G S T C V A N S L G S C S \* S V T  
 Q G W E E H A S Q T L W G L A A E V S Q  
 K A G R N M R R K L F G V L R L K C H S -  
  
 GCTCTTTTCTGCTATTTCACGCTCAACAGCGCTTCACAGCGCTGTGACCAAGCATCTAGACGA  
 3001 ----- 3060  
 CGGACAGACAGCTTAACGCTTCACITGTCGGAGGCTCTGTCACAGCGCTGTGTAGATGTGT  
  
 A C F W I C R \* T A S K K C A F T E T K -  
 P V S C F A G E Q F P D G V H Q H L Q D -  
 L F L D L Q V N S L Q T V C T N I Y K I -  
  
 TCTCTTCTGCTCAAGGCTACAGGTTTCACGCGTGTGTGCTGAGCTGCCATTCTATGAGC  
 3061 ----- 3120  
 AGGAGCAGCAGCTCCGATGTTCAAGTGTGTACACAGCAGCTGAGGCTAAAGTAGTGT  
  
 S S C C R R T G F T H V C C E S H F I S -  
 P F A A G V Q V S R M C A A A P I S S A -  
 L L L Q A Y R F H A C V L O L P F H Q Q -  
  
 AAGTTTGAAGAAGCCACATTTTCTGCGGCTGATCTCTACAGCGCTCTCTCTCTCT  
 3121 ----- 3180  
 TTCAGACCTTCTTGGGCTGTAAAAAGCAGCCCACTACAGACTCTGCGCGAGCGAGCGA  
  
 K F G R T P H F S C A S S L T R P F S A -  
 S L E E P H I F P A R H L \* H G L P L L  
 V W K N P T F F L R V I S D T A S L C Y  
  
 ACTGCTCTCTGAAGCCCAACAGCGCGATCTGCGCTGGGGGCAAGGGGXXXXXGCGCG  
 3181 ----- 3240  
 TTAGGTAGAGACTTCTCTCTCTCTCTCTACAGCGAGCGCGCTTCTGCGCGCGCGCG  
  
 T P S \* K F R T Q G C R W G P R A F P A -  
 L H F E S Q E R P D V A G G Q G R R R P -  
 S I L K A E N A G M S L C A K C A A C P -  
  
 CTCTGCTCTGAGAGCGCTGAGTGTGTGTGACAGCAAGCATTCCTGCTTAAAGTGAATC  
 3241 ----- 3300  
 GAGACCGGAGGCTTCTGCGAGCTTACCTACAGCGCTTCTTCTTAAAGTGAAGTGAAGTGA  
  
 L E P P P P C S G C A T K H S C S S \* L -  
 S A L E R G R A V A V P P S I P A Q A D S -  
 L P S E A V Q W L C H Q A F L L K L T R -  
  
 GACACGCTCTACCTAGCTGCGCTCTGCGGTGACTTACAGCAGCGCTAGACGCTAGCTTA  
 3301 ----- 3360  
 CTCTGTCACAGCTGATTCACGCTTACGAGCGCTACTGAGTGTCTTCTGCGGTCTGCGGTGAGT  
  
 D T V S P T C H S W G H S G Q F R R S \* -  
 T P C H L R A T P G V T O D S P D A A E -  
 H R V T Y V F L L G S L E T A Q T Q L S -

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[illegible]

Figure 72 (cont.)

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3781  TTTGGTATTGTTTACAGGCTGTGGCTTGGCTTTTGGCTTGGAGCCGAGGATCCAGGTT
----- 3840
AAGCGTAAACAAGTGTGGAGCGGACCGCAAGCAAAACGTAAGTGTGGGTTGGTAGGTTGAC

A   F A I V H F S P C P L F S T P T I Q V -
D   S E L F T P R F A L L C L P F F F S R W -
C   R H C S P L A L P S F A F H P H H P C G -

3841  GAGTCTTACAGGAGCGCTGTGGAGCTTGTGGAAATTGTGAGTGAACAGAGGTTTCCCTG
----- 3900
CTCTGAACTCTTCTCTGGGAGCTTGGAGAGCTTTAAAGCTGACTGGTTTTCAGCAAGGAG

A   E T L K S T L G A L G I W S D Q R C A L -
D   F P * E G P W E I W E F G V T K G V P C -
C   D P E K D G G S E C N L E * P K V C P V -

3901  TACACAGGCGAGGACCCCTGCACTGGAATGGGATTTCTGTGGCTCAAAATTGGGAGAGAT
----- 3960
ATCTCTCCGCTCTCTGGAGCTTGGAGCTTACCCCTCAGGACAGCTAGTTTAACCGCTCTGA

A   Y T G E D P A P G W G S L W V K L G G C -
D   T Q A R T L H L D G G P C G S N W G R V -
C   H R K C P C T W M C V P V C Q I G G E C

3961  GCTGTGGAGTAAATCTGAATATATGAGTTTTTTCATTTTCAAAAAAAAAAAAAAAAAA
----- 4020
CCACACCTCTATTTTATGACTTATATACTCAAAAAGTCAAAATTTTTTTTTTTTTTTT

A   A V G V K Y * I Y E F F S P E K K K K K
D   L W E * N T E Y M S F S V L K K K K K K
C   C G S K T L N I * V P Q F * K K K K K K -

4021  AAAAAAAAA
----- 4029
TTTTTTTTT

A   K K K -
D   K K -
C   K K -

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Figure 73

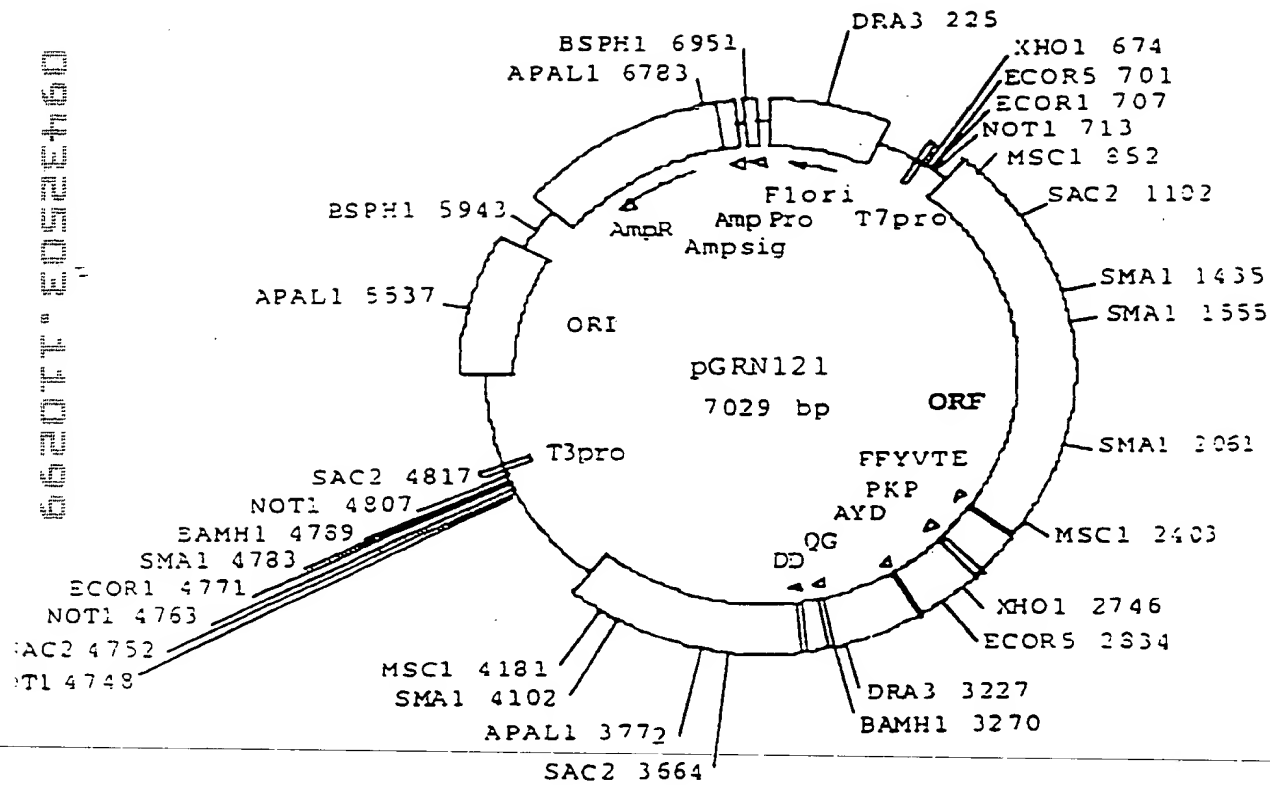


Figure 74

GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCG ATG

1  
met

10  
pro arg ala pro arg cys arg ala val arg ser leu leu arg ser  
CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC

20  
his tyr arg glu val leu pro leu ala thr phe val arg arg leu  
CAC TAC CGC GAG GTG CTG CCG CTG GCC ACC TTC GTG CGG CGC CTG

30  
gly pro gln gly trp arg leu val gln arg gly asp pro ala ala  
GGG CCC CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT

40  
phe arg ala leu val ala gln cys leu val cys val pro trp asp  
TTC CGC GCG CTG GTG GCC CAG TGC CTG GTG TCC GTG CCC TGG GAC

50  
ala arg pro pro pro ala ala pro ser phe arg gln val ser cys  
GCA CGG CCG CCC CCC GCC GCC CCC TCC TTC CGC CAG GTG TCC TGC

60  
leu lys glu leu val ala arg val leu gln arg leu cys glu arg  
CTG AAG GAG CTG GTG GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC

70  
gly ala lys asn val leu ala phe gly phe ala leu leu asp gly  
GGC GCG AAG AAC GTG CTG GCC TTC GGC TTC GCG CTG CTG GAC GGG

80  
ala arg gly gly pro pro glu ala phe thr thr ser val arg ser  
GCC CGC GGG GGC CCC CCC GAG GCC TTC ACC ACC AGC GTG CGC AGC

90  
tyr leu pro asn thr val thr asp ala leu arg gly ser gly ala  
TAC CTG CCC AAC ACG GTG ACC GAC GCA CTG CGG GGG AGC GGG GCG

100  
110  
120  
130

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Figure 74 (cont.)

			290											300		
gly	ala	leu	ser	gly	thr	arg	his	ser	his	pro	ser	val	gly	arg		
CGT	GCG	CTC	TCT	GGC	ACG	CGC	CAC	TCC	CAC	CCA	TCC	GTG	GGC	CGC		
								310								
gln	his	his	ala	gly	pro	pro	ser	thr	ser	arg	pro	pro	arg	pro		
CAG	CAC	CAC	GCG	GGC	CCC	CCA	TCC	ACA	TCG	CGG	CCA	CCA	CGT	CCC		
			320												330	
trp	asp	thr	pro	cys	pro	pro	val	tyr	ala	glu	thr	lys	his	phe		
TGG	GAC	ACG	CCT	TGT	CCC	CCG	GTG	TAC	GCC	GAG	ACC	AAG	CAC	TTC		
								340								
leu	tyr	ser	ser	gly	asp	lys	glu	gln	leu	arg	pro	ser	phe	leu		
CTC	TAC	TCC	TCA	GGC	GAC	AAG	GAG	CAG	CTG	CGG	CCC	TCC	TTC	CTA		
			350												360	
leu	ser	ser	ala	gly	ala	arg	arg	leu	val							
CTC	AGC	TCT	CTG	AGG	GCT	CGG	AGG	CTC	GTG							
								370								
glu	thr	ile	phe	leu	gly	ser	arg	pro	trp	met	pro	gly	thr	pro		
GAG	ACC	ATC	TTT	CTG	GGT	TCC	AGG	CCC	TGG	ATG	CCA	GGG	ACT	CCC		
			380												390	
arg	arg	leu	pro	arg	leu	pro	gln	arg	tyr	trp	gln	met	arg	pro		
CGC	AGG	TTG	CCC	CGC	CTG	CCC	CAG	CGC	TAC	TGG	CAA	ATG	CGG	CCC		
								400								
leu	phe	leu	glu	leu	leu	gly	asn	his	ala	gln	cys	pro	tyr	gly		
CTG	TTT	CTG	GAG	CTG	CTT	GGG	AAC	CAC	GCG	CAG	TGC	CCC	TAC	GGG		
			410												420	
val	leu	leu	lys	thr	his	cys	pro	leu	arg	ala	ala	val	thr	pro		
GTG	CTC	CTC	AAG	ACG	CAC	TGC	CCG	CTG	CGA	GCT	GCG	GTC	ACC	CCA		
								430								
ala	ala	gly	val	cys	ala	arg	glu	lys	pro	gln	gly	ser	val	ala		
GCA	GCC	GGT	GTC	TGT	GCC	CGG	GAG	AAG	CCC	CAG	GCC	TCT	GTG	GCG		

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[illegible]

440														450	
ala	pro	glu	glu	glu	asp	thr	asp	pro	arg	arg	leu	val	gln	leu	
GCC	CCC	GAG	GAG	GAG	GAC	ACA	GAC	CCC	CGT	CGC	CTG	GTG	CAG	CTG	
460														480	
leu	arg	gln	his	ser	ser	pro	trp	gln	val	tyr	gly	phe	val	arg	
CTC	CGC	CAG	CAC	AGC	AGC	CCC	TGG	CAG	GTG	TAC	CGC	TTC	GTG	CGG	
470														490	
ala	cys	leu	arg	arg	leu	val	pro	pro	gly	leu	trp	gly	ser	arg	
GCC	TGC	CTG	CGC	CGG	CTG	GTG	CCC	CCA	GGC	CTC	TGG	GGC	TCC	AGG	
500														510	
his	asn	glu	arg	arg	phe	leu	arg	asn	thr	lys	lys	phe	ile	ser	
CAC	AAC	GAA	CGC	CGC	TTC	CTC	AGG	AAC	ACC	AAG	AAG	TTC	ATC	TCC	
520														540	
leu	gly	lys	his	ala	lys	leu	ser	leu	gln	glu	leu	thr	trp	lys	
CTG	GGG	AAG	CAT	GCC	AAG	CTC	TCG	CTG	CAG	GAG	CTG	ACG	TGG	AAG	
530														550	
met	ser	val	arg	asp	cys	ala	trp	leu	arg	arg	ser	pro	gly	val	
ATG	AGC	GTG	CGG	GAC	TGC	GCT	TGG	CTG	CGC	AGG	AGC	CCA	GGG	GTT	
560														580	
gly	cys	val	pro	ala	ala	glu	his	arg	leu	arg	glu	glu	ile	leu	
GGC	TGT	GTT	CCG	GCC	GCA	GAG	CAC	CGT	CTG	CGT	GAG	GAG	ATC	CTG	
590														600	
ala	lys	phe	leu	his	trp	leu	met	ser	val	tyr	val	val	glu	leu	
GCC	AAG	TTC	CTG	CAC	TGG	CTG	ATG	AGT	GTG	TAC	GTC	GTC	GAG	CTG	
610														630	
leu	arg	ser	phe	phe	tyr	val	thr	glu	thr	thr	phe	gln	lys	asn	
CTC	AGG	TCT	TTC	TTT	TAT	GTC	ACG	GAG	ACC	ACG	TTT	CAA	AAG	AAC	
640														660	
arg	leu	phe	phe	tyr	arg	pro	ser	val	trp	ser	lys	leu	gln	ser	
AGG	CTC	TTT	TTC	TAC	CGG	CCG	AGT	GTC	TGG	AGC	AAG	TTG	CAA	AGC	
670														690	
ile	gly	ile	arg	gln	his	leu	lys	arg	val	gln	leu	arg	glu	leu	
ATT	GGA	ATC	AGA	CAG	CAC	TTG	AAG	AGG	GTG	CAG	CTG	CGG	GAG	CTG	

Figure 74 (cont.)

610  
 ser glu ala glu val arg gln his arg glu ala arg pro ala leu  
 TCG GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG

620  
 leu thr ser arg leu arg phe ile pro lys pro asp gly leu arg  
 CTG ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG

640  
 pro ile val asn met asp tyr val val gly ala arg thr phe arg  
 CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC

650  
 arg glu lys arg ala glu arg leu thr ser arg val lys ala leu  
 AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG

670  
 phe ser val leu asn tyr glu arg ala arg arg pro gly leu leu  
 TTC ACC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC GGC CTC CTG

680  
 gly ala ser val leu gly leu asp asp ile his arg ala trp arg  
 GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC

700  
 thr phe val leu arg val arg ala gln asp pro pro pro glu leu  
 ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG CTG

710  
 tyr phe val lys val asp val thr gly ala tyr asp thr ile pro  
 TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC

730  
 gln asp arg leu thr glu val ile ala ser ile ile lys pro gln  
 CAG GAC AGG CTC ACC GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG

740  
 asn thr tyr cys val arg arg tyr ala val val gln lys ala ala  
 AAC ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC

760  
 his gly his val arg lys ala phe lys ser his val ser thr leu  
 CAT GGG CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC TCT ACC TTG

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Figure 74 (cont.)

			770											780	
thr	asp	leu	gln	pro	tyr	met	arg	gln	phe	val	ala	his	leu	gln	
ACA	GAC	CTC	CAG	CCG	TAC	ATG	CGA	CAG	TTC	GTG	GCT	CAC	CTG	CAG	
								790							
glu	thr	ser	pro	leu	arg	asp	ala	val	val	ile	glu	gln	ser	ser	
GAG	ACC	AGC	CCG	CTG	AGG	GAT	GCC	GTC	GTC	ATC	GAG	CAG	AGC	TCC	
			800											810	
ser	leu	asn	glu	ala	ser	ser	gly	leu	phe	asp	val	phe	leu	arg	
TCC	CTG	AAT	GAG	GCC	AGC	AGT	GGC	CTC	TTC	GAC	GTC	TTC	CTA	CGC	
								820							
phe	met	cys	his	his	ala	val	arg	ile	arg	gly	lys	ser	tyr	val	
TTC	ATG	TGC	CAC	CAC	GCC	GTG	CGC	ATC	AGG	GGC	AAG	TCC	TAC	GTC	
			830											840	
gln	cys	gln	gly	ile	pro	gln	gly	ser	ile	leu	ser	thr	leu	leu	
CAG	TGC	CAG	GGG	ATC	CCG	CAG	GGC	TCC	ATC	CTC	TCC	ACG	CTG	CTC	
								850							
cys	ser	leu	cys	tyr	gly	asp	met	glu	asn	lys	leu	phe	ala	gly	
TGC	AGC	CTG	TGC	TAC	GGC	GAC	ATG	GAG	AAC	AAG	CTG	TTT	GCG	GGG	
			860											870	
ile	arg	arg	asp	gly	leu	leu	leu	arg	leu	val	asp	asp	phe	leu	
ATT	CCG	CGG	GAC	GGG	CTG	CTC	CTG	CGT	TTG	GTG	GAT	GAT	TTC	TTG	
								880							
leu	val	thr	pro	his	leu	thr	his	ala	lys	thr	phe	leu	arg	thr	
TTG	GTG	ACA	CCT	CAC	CTC	ACC	CAC	GCG	AAA	ACC	TTC	CTC	AGG	ACC	
			890											900	
leu	val	arg	gly	val	pro	glu	tyr	gly	cys	val	val	asn	leu	arg	
CTG	GTG	CGA	GGT	GTC	CCT	GAG	TAT	GGC	TGC	GTG	GTG	AAC	TTG	CGG	
								910							
lys	thr	val	val	asn	phe	pro	val	glu	asp	glu	ala	leu	gly	gly	
AAG	ACA	GTG	GTG	AAC	TTC	CCT	GTA	GAA	GAC	GAG	GCC	CTG	GGT	GCG	
			920											930	
thr	ala	phe	val	gln	met	pro	ala	his	gly	leu	phe	pro	trp	cys	
ACG	GCT	TTT	GTT	CAG	ATG	CCG	GCC	CAC	GGC	CTA	TTC	CCC	TGG	TGC	

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Figure 74 (cont.)

940  
gly leu leu leu asp thr arg thr leu glu val gln ser asp tyr  
GGC CTG CTG CTG GAT ACC CGG ACC CTG GAG GTG CAG AGC GAC TAC

950  
ser ser tyr ala arg thr ser ile arg ala ser val thr phe asn  
TCC AGC TAT GCC CGG ACC TCC ATC AGA GCC AGT GTC ACC TTC AAC

960  
arg gly phe lys ala gly arg asn met arg arg lys leu phe gly  
CGC GGC TTC AAG GCT GGG AGG AAC ATG CGT CGC AAA CTC TTT GGG

970  
val leu arg leu lys cys his ser leu phe leu asp leu gln val  
GTC TTG CGG CTG AAG TGT CAC AGC CTG TTT CTG GAT TTG CAG GTG

980  
asn ser leu gln thr val cys thr asn ile tyr lys ile leu leu  
AAC AGC CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG

990  
leu gln ala tyr arg phe his ala cys val leu gln leu pro phe  
CTG CAG GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT

1000  
his gln gln val trp lys asn pro thr phe phe leu arg val ile  
CAT CAG CAA GTT TGG AAG AAC CCC ACA TTT TTC CTG CGC GTC ATC

1010  
ser asp thr ala ser leu cys tyr ser ile leu lys ala lys asn  
TCT GAC ACG GCC TCC CTC TGC TAC TCC ATC CTG AAA GCC AAG AAC

1020  
ala gly met ser leu gly ala lys gly ala ala gly pro leu pro  
GCA GCG ATG TCG CTG GGG GCC AAG GGC GCC GCC GGC CCT CTG CCC

1030  
ser glu ala val gln trp leu cys his gln ala phe leu leu lys  
TCC GAG GCC GTG CAG TGG CTG TGC CAC CAA GCA TTC CTG CTC AAG

1040  
leu thr arg his arg val thr tyr val pro leu leu gly ser leu  
CTG ACT CGA CAC CGT GTC ACC TAC GTG CCA CTC CTG GGG TCA CTC

1050  
1060  
1070  
1080  
1090

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Figure 74 (cont.)

1100 1110  
arg thr ala gln thr gln leu ser arg lys leu pro gly thr thr  
AGG ACA GCC CAG ACG CAG CTG AGT CGG AAG CTC CCG GGG ACG ACG

1120  
leu thr ala leu glu ala ala ala asn pro ala leu pro ser asp  
CTG ACT GCC CTG GAG GCC GCA GCC AAC CCG GCA CTG CCC TCA GAC

1130 1132  
phe lys thr ile leu asp OP  
TTC AAG ACC ATC CTG GAC TGA TGGCCACCCGCCACAGCCAGGCCGAGAGCAGA

CACCAGCAGCCCTGTACGCCGGGCTCTACGTCCCAGGGAGGGAGGGGGCGGCCACACCC  
AGGCCCGCACCCTGAGGAGTCTGAGGCCTGAGTGAGTGTTTGGCCGAGGCCTGCATGTCC  
GGCTGAAGGCTGAGTGTCGGGCTGAGGCCTGAGCGAGTGTCAGCCAAGGGCTGAGTGTC  
CAGCACACCTGCCGTCTTACCTTCCACAGGCTGGCGCTCGGCTCCACCCCAGGGCCAG  
CTTTTCYTACCCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCCAGATT  
CGCCATTGTTACCCYTCGCCCTGCCYTCCTTTGCCTTCCACCCCCACCATCCAGGTGGA  
GACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTGCCCTGTA  
CACAGGCGAGGACCCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGGGAGGTGC  
TGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTTGRAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAA

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66207F E052E460

Figure 75

KPN1 17050  
KPN1 18560  
ECOR1 19475  
SAC1 19652  
SAC1 21083  
ECOR1 22539  
SAC1 24607  
SAC1 29043

<-TCP

66207E 0952E460